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From: Jiang, Dong
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Thank you very much.

Dong Jiang (78243)

703-305-1345

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Art Unit 1646

dong.jiang@uspto.gov

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Full text: _____
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 10.8103 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	77.8	92	2	US-08-273-146-45
2	42	77.8	92	2	US-08-273-146-53
3	42	77.8	107	2	US-08-888-366-14
4	42	77.8	107	2	US-08-888-366-20
5	42	77.8	107	2	US-08-888-366-26
6	42	77.8	109	2	US-08-713-939A-74
7	42	77.8	109	4	US-09-036-579-74
8	42	77.8	109	4	US-09-550-374-74
9	39	72.2	107	3	US-08-483-749A-26
10	39	72.2	243	1	US-08-133-804-6
11	39	72.2	243	1	US-08-461-838-6
12	39	72.2	243	2	US-08-461-838-6
13	39	72.2	243	2	US-08-356-786-4
14	39	72.2	534	2	US-08-356-786-10
15	38	70.4	95	2	US-08-713-939A-72
16	38	70.4	95	4	US-09-036-579-72
17	38	70.4	95	4	US-09-550-374-72
18	38	70.4	109	2	US-08-713-939A-73
19	38	70.4	109	4	US-09-036-579-73
20	38	70.4	109	4	US-09-550-374-73
21	38	70.4	145	4	US-09-096-244-2
22	35	64.8	11	1	US-07-942-245-497
23	35	64.8	31	4	US-08-525-539A-3
24	35	64.8	107	1	US-08-436-463-20
25	35	64.8	107	1	US-08-107-669D-1
26	35	64.8	107	1	US-08-472-788A-1
27	35	64.8	107	2	US-08-477-531B-1

28	35	64.8	107	2	US-08-082-842A-1	Sequence 1, Appli
29	35	64.8	109	1	US-07-942-245-4	Sequence 4, Appli
30	34	63.0	11	1	US-08-137-117D-117	Sequence 117, App
31	34	63.0	11	2	US-08-436-717-117	Sequence 117, App
32	34	63.0	51	1	US-08-472-788A-73	Sequence 73, Appl
33	34	63.0	51	1	US-08-472-788A-74	Sequence 74, Appl
34	34	63.0	51	2	US-08-082-842A-73	Sequence 73, Appl
35	34	63.0	51	2	US-08-082-842A-74	Sequence 74, Appl
36	34	63.0	107	1	US-07-634-278-50	Sequence 50, Appl
37	34	63.0	107	1	US-07-634-278-51	Sequence 51, Appl
38	34	63.0	107	1	US-08-477-728-50	Sequence 50, Appl
39	34	63.0	107	1	US-08-477-728-51	Sequence 51, Appl
40	34	63.0	107	1	US-08-425-336-125	Sequence 125, App
41	34	63.0	107	1	US-08-474-040-50	Sequence 50, Appl
42	34	63.0	107	1	US-08-474-040-51	Sequence 51, Appl
43	34	63.0	107	1	US-08-487-200-50	Sequence 50, Appl
44	34	63.0	107	1	US-08-487-200-51	Sequence 51, Appl
45	34	63.0	107	1	US-08-488-113B-125	Sequence 125, App

ALIGNMENTS

RESULT 1
US-08-273-146-45
; Sequence 45, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-45

Query Match 77.8% ; Score 42; ; DB 2; ; Length 92;
Best Local Similarity 90.0% ; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKL 10
| | | | | | | |
Db 16 RASQDIGSSL 25

RESULT 2

US-08-273-146-53
; Sequence 53, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kanten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994

CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771

REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158

INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-273-146-53

Query Match 77.8%; Score 42; DB 2; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKL 10
| | | | | | | |
Db 16 RASQDIGSSL 25

RESULT 3

US-08-888-366-14
; Sequence 14, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore

NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989

ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093

REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-888-366-14

Query Match 77.8%; Score 42; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 4

US-08-888-366-20
; Sequence 20, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo

APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo

NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.

CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible


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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-20

Query Match 77.8%; Score 42; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 24 RASQDIGSSL 33

RESULT 5
US-08-888-366-26
; Sequence 26, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
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; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-26

Query Match 77.8%; Score 42; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 24 RASQDIGSSL 33

RESULT 6
US-08-713-939A-74
; Sequence 74, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match 77.8%; Score 42; DB 2; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 7

US-09-036-579-74
; Sequence 74, Application US/09036579
; Patent No. 6290954

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,579
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,939
; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-036-579-74

Query Match 77.8%; Score 42; DB 4; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 8

US-09-550-374-74
; Sequence 74, Application US/09550374
; Patent No. 6372214

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/550,374
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/036,579
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-550-374-74

Query Match 77.8%; Score 42; DB 4; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKL 10
| | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 9

US-08-483-749A-26

; Sequence 26, Application US/08483749A
; Patent No. 6054561

; GENERAL INFORMATION:

; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA

; ZIP: 94662-8097

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A

; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SAVERIDE, PAUL B.
 ; REGISTRATION NUMBER: 36,914
 ; REFERENCE/DOCKET NUMBER: 0508.008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 601-2585
 ; TELEFAX: (510) 655-3542
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-749A-26

Query Match 72.2%; Score 39; DB 3; Length 107;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
 Db 24 RASQDIGNSL 33

RESULT 10
 ; US-08-133-804-6
 ; Sequence 6, Application US/08133804
 ; Patent No. 5534254
 ; GENERAL INFORMATION:
 ; APPLICANT: Huston, James S.
 ; APPLICANT: Oppermann, Hermann
 ; APPLICANT: Houston, L. L.
 ; APPLICANT: Ring, David B.
 ; TITLE OF INVENTION: Biosynthetic Binding Proteins For
 ; TITLE OF INVENTION: Imaging
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
 ; STREET: Exchange Place, 53 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/133,804
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kelley, Robin D.
 ; REGISTRATION NUMBER: 34,637
 ; REFERENCE/DOCKET NUMBER: 2054/22
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-248-7477
 ; TELEFAX: 617-248-7100
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 243 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-133-804-6

Query Match 72.2%; Score 39; DB 1; Length 243;
 Best Local Similarity 80.0%; Pred. No. 2.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
 Db 157 RASQDIGNSL 166

RESULT 11
 ; US-08-461-838-6
 ; Sequence 6, Application US/08461838
 ; Patent No. 5753204
 ; GENERAL INFORMATION:
 ; APPLICANT: Huston, James S.
 ; APPLICANT: Oppermann, Hermann
 ; APPLICANT: Houston, L. L.
 ; APPLICANT: Ring, David B.
 ; TITLE OF INVENTION: Biosynthetic Binding Proteins For
 ; TITLE OF INVENTION: Imaging
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
 ; STREET: Exchange Place, 53 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/461,838
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kelley, Robin D.
 ; REGISTRATION NUMBER: 34,637
 ; REFERENCE/DOCKET NUMBER: 2054/22
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-248-7477
 ; TELEFAX: 617-248-7100
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 243 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-461-838-6

Query Match 72.2%; Score 39; DB 1; Length 243;
 Best Local Similarity 80.0%; Pred. No. 2.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
 Db 157 RASQDIGNSL 166

RESULT 12
 ; US-08-461-386-6
 ; Sequence 6, Application US/08461386
 ; Patent No. 5837846
 ; GENERAL INFORMATION:
 ; APPLICANT: Huston, James S.
 ; APPLICANT: Oppermann, Hermann
 ; APPLICANT: Houston, L. L.
 ; APPLICANT: Ring, David B.
 ; TITLE OF INVENTION: Biosynthetic Binding Proteins For
 ; TITLE OF INVENTION: Imaging
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
 ; STREET: Exchange Place, 53 State Street
 ; CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-386-6

Query Match 72.2%; Score 39; DB 2; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
Db 157 RASQDIGNSL 166
RESULT 13
US-08-356-786-4
Sequence 4, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELEPHONE: (617) 248-7000

Query Match 72.2%; Score 39; DB 2; Length 243;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
Db 448 RASQDIGNSL 457

TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-4

Query Match 72.2%; Score 39; DB 2; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
Db 157 RASQDIGNSL 166

RESULT 14
US-08-356-786-10
Sequence 10, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-10

Query Match 72.2%; Score 39; DB 2; Length 534;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 10
Db 448 RASQDIGNSL 457

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RESULT 15
US-08-713-939A-72
; Sequence 72, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,939A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX:
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-713-939A-72

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Query Match          70.4%; Score 38; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 RASQDIGSKL 10
    |||||
Db 10 RASQDFGSSL 19

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Search completed: March 10, 2003, 17:02:30
Job time : 10.8103 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 6.87931 Seconds
(without alignments)
29,939 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues.

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pap.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pap.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pap.*
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6: /cgn2_6/ptodata/2/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	92	2	US-08-273-146-45
2	31	100.0	92	2	US-08-273-146-45
3	31	100.0	107	3	US-08-483-749A-26
4	31	100.0	109	1	US-08-466-886-27
5	31	100.0	109	2	US-08-713-939A-74
6	31	100.0	109	4	US-08-469-617-27
7	31	100.0	109	4	US-09-036-579-74
8	31	100.0	109	4	US-09-550-374-74
9	31	100.0	243	1	US-08-133-804-6
10	31	100.0	243	1	US-08-461-838-6
11	31	100.0	243	2	US-08-461-386-6
12	31	100.0	243	2	US-08-356-786-4
13	31	100.0	534	2	US-08-356-786-10
14	31	100.0	694	2	US-08-895-522-3
15	31	100.0	694	3	US-09-195-391-3
16	31	100.0	747	2	US-08-895-522-1
17	31	100.0	747	3	US-09-195-391-1
18	28	90.3	109	1	US-08-466-886-26
19	28	90.3	109	4	US-08-469-617-26
20	28	90.3	1307	1	US-08-395-246C-2
21	28	90.3	1334	2	US-08-996-545-2
22	28	90.3	1334	4	US-09-328-320-2
23	28	90.3	1349	2	US-08-612-734B-2
24	28	90.3	1408	1	US-08-612-521-2
25	27	87.1	105	4	US-08-881-189B-13
26	27	87.1	107	2	US-08-888-366-14
27	27	87.1	107	2	US-08-888-366-20

28	27	87.1	107	2	US-08-888-366-26	Sequence 26, Appl
29	27	87.1	591	4	US-09-199-290-7	Sequence 7, Appl
30	27	87.1	618	4	US-09-199-290-34	Sequence 34, Appl
31	26	83.9	400	4	US-08-961-083-190	Sequence 190, Appl
32	25	80.6	15	2	US-08-466-860-44	Sequence 44, Appl
33	25	80.6	15	3	US-08-472-040A-44	Sequence 44, Appl
34	25	80.6	15	4	US-08-276-776-44	Sequence 44, Appl
35	25	80.6	15	4	US-08-471-209-44	Sequence 44, Appl
36	25	80.6	107	4	US-09-240-274-29	Sequence 29, Appl
37	25	80.6	109	1	US-08-466-886-24	Sequence 24, Appl
38	25	80.6	109	4	US-08-469-617-24	Sequence 24, Appl
39	25	80.6	110	1	US-08-466-886-20	Sequence 20, Appl
40	25	80.6	110	1	US-08-466-886-21	Sequence 21, Appl
41	25	80.6	110	1	US-08-466-886-22	Sequence 22, Appl
42	25	80.6	110	1	US-08-466-886-23	Sequence 23, Appl
43	25	80.6	110	1	US-08-466-886-25	Sequence 25, Appl
44	25	80.6	110	4	US-08-469-617-20	Sequence 20, Appl
45	25	80.6	110	4	US-08-469-617-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-273-146-45
; Sequence 45, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-45

Query Match 100.0%; Score 31; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
 Db 42 ATSSLDS 48

RESULT 2

US-08-273-146-53
 ; Sequence 53, Application US/08273146
 ; Patent No. 5855885
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Roger
 ; APPLICANT: McCafferty, John
 ; APPLICANT: Chiswell, David
 ; APPLICANT: Darsley, Michael J.
 ; APPLICANT: Fitzgerald, Kevin
 ; APPLICANT: Kenten, John H.
 ; APPLICANT: Martin, Mark T.
 ; APPLICANT: Titmas, Richard C.
 ; APPLICANT: Williams, Richard O.
 ; TITLE OF INVENTION: The Isolation and Production of
 ; TITLE OF INVENTION: Catalytic Antibodies using Phage technology
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IGEN, Inc.
 ; STREET: 1530 East Jefferson St.
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20852

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/273,146
 FILING DATE: 14-JUL-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ryan, John W.
 REGISTRATION NUMBER: 33,771
 REFERENCE/DOCKET NUMBER: 09000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-984-8000
 TELEFAX: 301-230-0158
 INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-273-146-53

Query Match 100.0%; Score 31; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
 Db 42 ATSSLDS 48

RESULT 3

US-08-483-749A-26
 ; Sequence 26, Application US/08483749A
 ; Patent No. 6054561
 ; GENERAL INFORMATION:
 ; APPLICANT: RING, DAVID B.
 ; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
 ; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 ; NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION
 STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
 CITY: EMERYVILLE
 STATE: CA

COUNTRY: USA
 ZIP: 94662-8097

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,749A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: SAVEREIDE, PAUL B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0508.008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2585
 TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-483-749A-26

Query Match 100.0%; Score 31; DB 3; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
 Db 50 ATSSLDS 56

RESULT 4

US-08-466-886-27
 ; Sequence 27, Application US/08466886
 ; Patent No. 5776677

GENERAL INFORMATION:

APPLICANT: Tsui, Lap-Chee
 APPLICANT: Riordan, John R.
 APPLICANT: Rommens, Johanna M.
 APPLICANT: Kerem, Bat-Sheva
 APPLICANT: Collins, Francis S.
 APPLICANT: Iannuzzi, Michael C.
 APPLICANT: Drumm, Mitchell L.
 APPLICANT: Buckwald, Manuel

TITLE OF INVENTION: Cystic Fibrosis Gene
 NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,886
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldstein, Jorge A.

REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.0010006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-466-886-27

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 99 ATSSLS 105

RESULT 5
US-08-713-939A-74
Sequence 74, Application US/08713939A
Patent No. 5846533

GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 50 ATSSLS 56

RESULT 6
US-08-469-617-27
Sequence 27, Application US/08469617
Patent No. 6201107

GENERAL INFORMATION:
APPLICANT: Tsui, Lap-Chee
APPLICANT: Riordan, John R.
APPLICANT: Rommens, Johanna M.
APPLICANT: Kerem, Bat-Sheva
APPLICANT: Collins, Francis S.
APPLICANT: Iannuzzi, Michael C.
APPLICANT: Drumm, Mitchell L.
APPLICANT: Buckwald, Manuel
TITLE OF INVENTION: Cystic Fibrosis Gene
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,617
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.0010008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-469-617-27

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 99 ATSSLS 105

RESULT 7
US-09-036-579-74
Sequence 74, Application US/09036579
Patent No. 6290954

GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-579-74

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 8
US-09-550-374-74
Sequence 74, Application US/09550374
Patent No. 6372214
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,374
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-74

Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56

RESULT 9
US-08-133-804-6
Sequence 6, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-133-804-6

Query Match 100.0%; Score 31; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 9,7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

Db 183 ATSSLS 189
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RESULT 10

US-08-461-838-6

; Sequence 6, Application US/08461838

; Patent No. 5753204

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,838

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Kelley, Robin D.

; REGISTRATION NUMBER: 34,637

; REFERENCE/DOCKET NUMBER: 2054/22

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-248-7477

; TELEFAX: 617-248-7100

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 243 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-461-838-6

Query Match 100.0%; Score 31; DB 1; Length 243;

Best Local Similarity 100.0%; Pred. No. 9.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

|||||

Db 183 ATSSLS 189

RESULT 11

US-08-461-386-6

; Sequence 6, Application US/08461386

; Patent No. 5837846

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Testa, Hurwitz & Thibault/Patent Department

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-4

Query Match 100.0%; Score 31; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 183 ATSSLS 189

RESULT 13
US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 5877305

; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-10

Query Match 100.0%; Score 31; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 474 ATSSLS 480

RESULT 14

US-08-895-522-3
; Sequence 3, Application US/08895522
; Patent No. 5858719
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE
; TITLE OF INVENTION: TRANSPORT PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/895,522
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0336 US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1167982

US-08-895-522-3

Query Match 100.0%; Score 31; DB 2; Length 694;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 577 ATSSLS 583

RESULT 15

US-09-195-391-3
; Sequence 3, Application US/09195391
; Patent No. 6080842
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE
; TITLE OF INVENTION: TRANSPORT PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA

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; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,391
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/895,522
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0336 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1167982
; US-09-195-391-3

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Query Match      100.0%; Score 31; DB 3; Length 694;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSLDS 7
Db 577 ATSSLDS 583

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Search completed: March 10, 2003, 17:02:31
Job time : 7.87931 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 8.84483 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2.6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2.6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2.6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2.6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	92	2	US-08-273-146-45
2	47	100.0	92	2	US-08-273-146-53
3	47	100.0	145	4	US-09-096-244-2
4	42	89.4	109	2	US-08-713-939A-74
5	42	89.4	109	4	US-09-036-579-74
6	42	89.4	109	4	US-09-550-374-74
7	40	85.1	95	2	US-08-713-939A-72
8	40	85.1	95	4	US-09-036-579-72
9	40	85.1	95	4	US-09-550-374-72
10	40	85.1	109	2	US-08-713-939A-73
11	40	85.1	109	4	US-09-036-579-73
12	40	85.1	109	4	US-09-550-374-73
13	39	83.0	9	2	US-08-350-260A-503
14	37	78.7	107	1	US-08-276-852-87
15	37	78.7	107	1	US-08-899-575-87
16	37	78.7	107	1	US-08-899-575-87
17	37	78.7	107	5	PCT-US95-08743-87
18	36	76.6	108	1	US-08-276-852-99
19	36	76.6	108	1	US-08-899-575-99
20	36	76.6	108	1	US-08-899-575-99
21	36	76.6	108	5	PCT-US95-08743-99
22	36	76.6	109	4	US-09-025-769B-16
23	35	74.5	53	1	US-08-162-102C-44
24	35	74.5	107	3	US-08-483-749A-26
25	35	74.5	109	1	US-08-162-102C-24
26	35	74.5	109	5	PCT-US93-08786-24
27	35	74.5	243	1	US-08-133-804-6

28	35	74.5	243	1	US-08-461-838-6	Sequence 6, Appli
29	35	74.5	243	2	US-08-461-838-6	Sequence 6, Appli
30	35	74.5	243	2	US-08-356-786-4	Sequence 4, Appli
31	35	74.5	534	2	US-08-356-786-10	Sequence 10, Appli
32	34	72.3	108	4	US-09-240-274-178	Sequence 178, Appl
33	33	70.2	9	3	US-08-599-226-14	Sequence 14, Appl
34	33	70.2	9	4	US-09-125-098-14	Sequence 19, Appl
35	32	68.1	9	3	US-08-599-226-19	Sequence 19, Appl
36	32	68.1	9	4	US-09-125-098-19	Sequence 19, Appl
37	32	68.1	23	2	US-08-303-569B-9	Sequence 9, Appli
38	32	68.1	105	3	US-09-065-059-17	Sequence 17, Appl
39	32	68.1	107	2	US-08-561-521-6	Sequence 6, Appli
40	32	68.1	107	2	US-08-561-521-8	Sequence 8, Appli
41	32	68.1	107	2	US-08-652-558-34	Sequence 34, Appl
42	32	68.1	107	2	US-08-652-558-47	Sequence 47, Appl
43	32	68.1	107	2	US-08-318-157B-6	Sequence 6, Appli
44	32	68.1	107	2	US-08-888-366-14	Sequence 14, Appl
45	32	68.1	107	2	US-08-888-366-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-273-146-45
; Sequence 45, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Roger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kanten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-45

Query Match 100.0%; Score 47; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. NO. 0.026;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9
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 Db 81 LOYASSPYT 89

RESULT 2

US-08-273-146-53
 ; Sequence 53, Application US/08273146
 ; Patent No. 5855885
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Rodger
 ; APPLICANT: McCafferty, John
 ; APPLICANT: Chiswell, David
 ; APPLICANT: Darsley, Michael J.
 ; APPLICANT: Fitzgerald, Kevin
 ; APPLICANT: Kenten, John H.
 ; APPLICANT: Martin, Mark T.
 ; APPLICANT: Titmas, Richard C.
 ; APPLICANT: Williams, Richard O.
 ; TITLE OF INVENTION: The Isolation and Production of
 ; CATALYTIC ANTIBODIES USING PHAGE TECHNOLOGY
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IGEN, Inc.
 ; STREET: 1530 East Jefferson St.
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20852
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/273,146
 ; FILING DATE: 14-JUL-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ryan, John W.
 ; REGISTRATION NUMBER: 33,771
 ; REFERENCE/DOCKET NUMBER: 09000
 ; TELEPHONE: 301-984-8000
 ; TELEFAX: 301-230-0158
 ; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 92 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-273-146-53

Query Match 100.0%; Score 47; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9
 |||||
 Db 81 LOYASSPYT 89

RESULT 3

US-09-096-244-2
 ; Sequence 2, Application US/09096244
 ; Patent No. 6274143
 ; GENERAL INFORMATION:
 ; APPLICANT: Chatterjee, Malaya
 ; APPLICANT: Foon, Kenneth A.
 ; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
 ; TUMORS USING ANTI-IDIOTYPE ANTIBODY
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HMF-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10

NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/096,244
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Polizzi, Catherine M.
 REGISTRATION NUMBER: 40,130
 REFERENCE/DOCKET NUMBER: 30414-20006.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 145 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-096-244-2

Query Match 100.0%; Score 47; DB 4; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9
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 Db 109 LOYASSPYT 117

RESULT 4

US-08-713-939A-74
 ; Sequence 74, Application US/08713939A
 ; Patent No. 5846533
 ; GENERAL INFORMATION:
 ; APPLICANT: Prusiner, Stanley B.
 ; APPLICANT: Williamson, R. Anthony
 ; APPLICANT: Burton, Dennis R.
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 2200 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/713,939A
 ; FILING DATE: 13-SEP-1996
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bozicevic, Karl

REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-74

Query Match 89.4%; Score 42; DB 2; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
DB 89 LOYASSPWT 97

RESULT 5

US-09-036-579-74
Sequence 74, Application US/09036579
Patent No. 6290954

GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/036,579
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/713,939

FILING DATE: 13-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277

TELEFAX: 415-854-0875

TELEX:

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-036-579-74

Query Match 89.4%; Score 42; DB 4; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
DB 89 LOYASSPWT 97

RESULT 6

US-09-550-374-74
Sequence 74, Application US/09550374
Patent No. 6372214

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

APPLICANT: Williamson, R. Anthony

APPLICANT: Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/550,374

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/036,579

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277

TELEFAX: 415-854-0875

TELEX:

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-550-374-74

Query Match 89.4%; Score 42; DB 4; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
DB 89 LOYASSPWT 97

RESULT 7

US-08-713-939A-72
Sequence 72, Application US/08713939A
Patent No. 5846533

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

APPLICANT: Williamson, R. Anthony

APPLICANT: Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-72

Query Match 85.1%; Score 40; DB 2; Length 95;
Best Local Similarity 77.8%; Pred. No. 0.64;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 75 LQYASSPYT 83

RESULT 8
US-09-036-579-72
Sequence 72, Application US/09036579
Patent No. 6290954
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-036-579-72

Query Match 85.1%; Score 40; DB 4; Length 95;
Best Local Similarity 77.8%; Pred. No. 0.64;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 75 LQYASSPYT 83

RESULT 9
US-09-550-374-72
Sequence 72, Application US/09550374
Patent No. 6372214
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,374
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-72

Query Match 85.1%; Score 40; DB 4; Length 95;
Best Local Similarity 77.8%; Pred. No. 0.64;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
||||:|:|
Db 75 LOYAAASPT 83

RESULT 10

US-08-713-939A-73
; Sequence 73, Application US/08713939A
; Patent No. 5845533

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08713,939A

; FILING DATE: 13-SEP-1996

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl

; REGISTRATION NUMBER: 28,807

; REFERENCE/DOCKET NUMBER: 06510/059001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-5277

; TELEFAX: 415-854-0875

; TELEX:

; INFORMATION FOR SEQ ID NO: 73:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-713-939A-73

Query Match 85.1%; Score 40; DB 2; Length 109;

Best Local Similarity 77.8%; Pred. No. 0.74;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
||||:|:|
Db 89 LOYAAASPT 97

RESULT 11

US-09-036-579-73

; Sequence 73, Application US/09036579

; Patent No. 6290954

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.

; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/036,579

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/713,939

; FILING DATE: 13-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl

; REGISTRATION NUMBER: 28,807

; REFERENCE/DOCKET NUMBER: 06510/059001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-5277

; TELEFAX: 415-854-0875

; TELEX:

; INFORMATION FOR SEQ ID NO: 73:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-036-579-73

Query Match 85.1%; Score 40; DB 4; Length 109;

Best Local Similarity 77.8%; Pred. No. 0.74;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
||||:|:|
Db 89 LOYAAASPT 97

RESULT 12

US-09-550-374-73

; Sequence 73, Application US/09550374

; Patent No. 637214

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.

; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/550,374

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/036,579

; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-550-374-73

Query Match 85.1%; Score 40; DB 4; Length 109;
Best Local Similarity 77.8%; Pred. No. 0.74;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
|||:|:|:
Db 89 LQYASSPYT 97

RESULT 13
US-08-350-260A-503
; Sequence 503, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 503:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-503
Query Match 83.0%; Score 39; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 QYASSPYT 9
|||:|:|:
Db 2 QYASSPYT 9
RESULT 14
US-08-276-852-87
; Sequence 87, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-87

Query Match 78.7%; Score 37; DB 1; Length 107;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 89 QYHSSPYT 96

RESULT 15
US-08-899-575-87
Sequence 87, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-87

Query Match 78.7%; Score 37; DB 1; Length 107;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 89 QYHSSPYT 96

Db 89 QYHSSPYT 96

Search completed: March 10, 2003, 17:02:31
Job time : 8.84483 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 8.91379 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues 188354
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	10	US-09-924-099-3
2	54	100.0	108	10	US-09-924-099-1
3	54	100.0	237	10	US-09-924-099-9
4	54	100.0	243	10	US-09-924-099-10
5	42	77.8	109	10	US-09-943-906-74
6	42	77.8	130	1	US-08-779-784-35
7	39	72.2	243	9	US-09-887-853-6
8	39	72.2	267	10	US-09-766-543-10
9	39	72.2	276	10	US-09-766-543-12
10	38	70.4	11	10	US-09-861-294-6
11	38	70.4	88	10	US-09-905-243-30
12	38	70.4	95	9	US-10-194-975-91
13	38	70.4	95	9	US-10-194-975-92
14	38	70.4	95	10	US-09-943-906-72
15	38	70.4	109	10	US-09-943-906-73
16	38	70.4	145	10	US-09-861-294-2
17	36	66.7	11	9	US-09-968-561A-298
18	36	66.7	11	10	US-09-192-854-170
19	35	64.8	31	9	US-09-956-206A-3

20	35	64.8	88	10	US-09-905-243-64	Sequence 64, Appl
21	34	63.0	118	10	US-09-811-737-4	Sequence 4, Appli
22	34	63.0	118	10	US-09-811-737-11	Sequence 11, Appl
23	34	63.0	244	10	US-09-940-391-1	Sequence 1, Appli
24	34	63.0	253	10	US-09-811-737-18	Sequence 18, Appl
25	34	63.0	255	10	US-09-811-737-15	Sequence 15, Appl
26	34	63.0	260	10	US-09-811-737-16	Sequence 16, Appl
27	34	63.0	260	10	US-09-811-737-17	Sequence 17, Appl
28	34	63.0	262	10	US-09-811-737-19	Sequence 19, Appl
29	34	63.0	324	10	US-09-815-242-14082	Sequence 14082, A
30	34	63.0	876	9	US-09-712-363-243	Sequence 243, App
31	33	61.1	11	10	US-09-798-058-8	Sequence 8, Appli
32	33	61.1	107	9	US-09-991-470-25	Sequence 25, Appl
33	33	61.1	109	10	US-09-798-058-4	Sequence 4, Appli
34	33	61.1	245	9	US-09-991-470-27	Sequence 27, Appl
35	33	61.1	312	9	US-09-789-054A-22	Sequence 22, Appl
36	33	61.1	315	10	US-09-764-853-772	Sequence 772, App
37	33	61.1	315	10	US-09-764-898-261	Sequence 261, App
38	33	61.1	348	9	US-09-789-054A-20	Sequence 20, Appl
39	33	61.1	348	10	US-09-764-898-188	Sequence 188, App
40	33	61.1	428	10	US-09-886-055-347	Sequence 347, App
41	32	59.3	11	10	US-09-253-794-20	Sequence 20, Appl
42	32	59.3	106	8	US-08-844-215-11	Sequence 11, Appl
43	32	59.3	106	10	US-09-253-794-4	Sequence 4, Appli
44	32	59.3	106	10	US-09-253-794-19	Sequence 19, Appl
45	32	59.3	107	10	US-09-756-301A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-924-099-3
; Sequence 3, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takao
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-3
Query Match 100.0%; Score 54; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQDIGSKLY 11
Db 1 RASQDIGSKLY 11
RESULT 2
US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takao

```
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match 100.0%; Score 54; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGSKLY 11
Db 24 RASODIGSKLY 34

RESULT 3
US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match 100.0%; Score 54; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGSKLY 11
Db 154 RASODIGSKLY 164

RESULT 4
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
```

```
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match 100.0%; Score 54; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASODIGSKLY 11
Db 154 RASODIGSKLY 164

RESULT 5
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match 77.8%; Score 42; DB 10; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 6
US-08-779-784-35
; Sequence 35, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYLINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-35

Query Match 77.8%; Score 42; DB 1; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 46 RASQDIGSSL 55

RESULT 7
US-09-887-853-6
; Sequence 6, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 72.2%; Score 39; DB 9; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 157 RASQDIGNSL 166

RESULT 8
US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543

; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520c9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match 72.2%; Score 39; DB 10; Length 267;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 185
||||||| I

RESULT 9

US-09-766-543-12
; Sequence 12, Application US/0976543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus
; OTHER INFORMATION: linker
US-09-766-543-12

Query Match 72.2%; Score 39; DB 10; Length 276;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 185
||||||| I

RESULT 10

US-09-861-294-6
; Sequence 6, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244

; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-6

Query Match 70.4%; Score 38; DB 10; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 11
||||||| I

Db 1 RASQDIGNSL 11

RESULT 11

US-09-905-243-30
; Sequence 30, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-905-243-30

Query Match 70.4%; Score 38; DB 10; Length 88;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNSL 11
||||||| I

Db 24 RASQDIGNSL 34

RESULT 12

US-10-194-975-91
; Sequence 91, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-194-975-91

Query Match 70.4%; Score 38; DB 9; Length 95;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
DB 24 RASQSIGSSLH 34

RESULT 13

US-10-194-975-92
; Sequence 92, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-92

Query Match 70.4%; Score 38; DB 9; Length 95;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
DB 24 RASQSIGSSLH 34

RESULT 14

US-09-943-906-72
; Sequence 72, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-943-906-72

Query Match 70.4%; Score 38; DB 10; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
DB 10 RASQDFGSSL 19

RESULT 15

US-09-943-906-73
; Sequence 73, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-943-906-73

Query Match 70.4%; Score 38; DB 10; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RASODIGSKL 10
| | | | |
Db 24 RASQDFGSSL 33

Search completed: March 10, 2003, 17:11:27
Job time : 8.91379 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 5.67241 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues
Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	31	100.0	7	10	US-09-924-099-4	Sequence 4, Appli
2	31	100.0	108	10	US-09-924-099-1	Sequence 1, Appli
3	31	100.0	109	10	US-09-943-906-74	Sequence 74, Appl
4	31	100.0	130	1	US-08-779-784-35	Sequence 35, Appl
5	31	100.0	237	10	US-09-924-099-9	Sequence 9, Appli
6	31	100.0	243	9	US-09-887-853-6	Sequence 6, Appli
7	31	100.0	243	10	US-09-924-099-10	Sequence 10, Appl
8	31	100.0	267	10	US-09-766-543-10	Sequence 10, Appl
9	31	100.0	276	10	US-09-766-543-12	Sequence 12, Appl
10	28	90.3	131	10	US-09-873-409-3	Sequence 3, Appli
11	28	90.3	327	10	US-09-815-242-11463	Sequence 11463, A
12	28	90.3	327	10	US-09-815-242-11625	Sequence 11625, A
13	28	90.3	514	10	US-09-873-409-8	Sequence 8, Appli
14	28	90.3	541	10	US-09-873-409-7	Sequence 7, Appli
15	28	90.3	812	10	US-09-873-409-2	Sequence 2, Appli
16	28	90.3	1058	10	US-09-873-409-4	Sequence 4, Appli
17	28	90.3	1195	10	US-09-873-409-6	Sequence 6, Appli
18	28	90.3	1222	10	US-09-873-409-5	Sequence 5, Appli
19	28	90.3	1334	9	US-09-758-828-2	Sequence 2, Appli

20	28	90.3	1394	9	US-10-101-388-3	Sequence 3, Appli
21	27	87.1	234	9	US-09-764-868-753	Sequence 753, App
22	27	87.1	271	10	US-09-901-884-4	Sequence 4, Appli
23	27	87.1	591	9	US-09-821-616-7	Sequence 7, Appli
24	27	87.1	618	9	US-09-821-616-34	Sequence 34, Appli
25	27	87.1	760	10	US-09-833-017-26	Sequence 26, Appli
26	27	87.1	848	10	US-09-839-185-8	Sequence 8, Appli
27	26	83.9	202	10	US-09-960-253-184	Sequence 184, App
28	26	83.9	400	10	US-09-765-272-190	Sequence 190, App
29	25	80.6	20	10	US-09-982-172-139	Sequence 139, App
30	25	80.6	25	10	US-09-982-172-67	Sequence 67, Appli
31	25	80.6	25	10	US-09-982-172-220	Sequence 220, App
32	25	80.6	107	9	US-09-848-798-29	Sequence 29, Appli
33	25	80.6	167	10	US-09-739-254-125	Sequence 125, App
34	25	80.6	167	10	US-09-904-615-125	Sequence 125, App
35	25	80.6	207	10	US-09-780-717-26	Sequence 26, Appli
36	25	80.6	223	12	US-10-062-254-204	Sequence 204, App
37	25	80.6	339	9	US-09-764-884-25	Sequence 25, Appli
38	25	80.6	351	9	US-10-021-811-10	Sequence 10, Appli
39	25	80.6	353	9	US-09-764-884-33	Sequence 33, Appli
40	25	80.6	458	10	US-09-737-149-28	Sequence 28, Appli
41	25	80.6	475	9	US-10-076-157-4	Sequence 4, Appli
42	25	80.6	501	10	US-09-815-242-13347	Sequence 13347, A
43	25	80.6	543	9	US-09-736-457-337	Sequence 337, App
44	25	80.6	543	9	US-09-902-941-337	Sequence 337, App
45	25	80.6	543	9	US-09-849-626-337	Sequence 337, App

ALIGNMENTS

RESULT 1
US-09-924-099-4
; Sequence 4, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-4

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 1 ATSSLDS 7

RESULT 2
US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori

```

; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match      100.0%; Score 31; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 50 ATSSLS 56

RESULT 3
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-943-906-74
Query Match      100.0%; Score 31; DB 10; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 50 ATSSLS 56

RESULT 4
US-08-779-784-35
; Sequence 35, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-35

Query Match      100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1' ATSSLS 7
Db 72 ATSSLS 78
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; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6
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Query Match 100.0%; Score 31; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 183 ATSSLDS 189

RESULT 7
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10
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Query Match 100.0%; Score 31; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 180 ATSSLDS 186

RESULT 8
US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543

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; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520C9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match 100.0%; Score 31; DB 10; Length 267;
Best Local Similarity 100.0%; Pred. No. 9.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 ATSSSLDS 7
Db 202 ATSSSLDS 208

RESULT 9
US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679,002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9Sfv plus
; OTHER INFORMATION: linker
US-09-766-543-12

Query Match 100.0%; Score 31; DB 10; Length 276;
Best Local Similarity 100.0%; Pred. No. 10; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 ATSSSLDS 7
Db 202 ATSSSLDS 208

RESULT 10
US-09-873-409-3
; Sequence 3, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3

; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-3

Query Match 90.3%; Score 28; DB 10; Length 131;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLDS 7
Db 106 ATSSSLDS 112

RESULT 11
US-09-815-242-11463
; Sequence 11463, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.Olia
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 11463
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11463

Query Match 90.3%; Score 28; DB 10; Length 327;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSLDS 7
Db 165 ATSSSLDS 171

RESULT 12
US-09-815-242-11625
; Sequence 11625, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.

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```

; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11625
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11625

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Query Match          90.3%; Score 28; DB 10; Length 327;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSILDS 7
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Db 165 ATSALDS 171

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RESULT 13
US-09-873-409-8
; Sequence 8, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873.409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-8

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Query Match          90.3%; Score 28; DB 10; Length 514;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSILDS 7
    |||:||||
Db 489 ATSALDS 495

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RESULT 14
US-09-873-409-7
; Sequence 7, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:

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; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873.409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: No. US20020037522A1e
; LOCATION: (230)-(230)
; OTHER INFORMATION: Xaa at position 230 represents any L amino acid
US-09-873-409-7

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Query Match          90.3%; Score 28; DB 10; Length 541;
Best Local Similarity 85.7%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSILDS 7
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Db 516 ATSALDS 522

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RESULT 15
US-09-873-409-2
; Sequence 2, Application US/09873409
; Patent No. US20020037522A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; APPLICANT: Sayegh, Mohamed
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268611
; CURRENT APPLICATION NUMBER: US/09/873.409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-409-2

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Query Match          90.3%; Score 28; DB 10; Length 812;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATSSILDS 7
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Db 106 ATSALDS 112

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Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LOYASSPYT 9

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	10	US-09-861-294-10
2	47	100.0	9	10	US-09-924-099-5
3	47	100.0	108	10	US-09-924-099-1
4	47	100.0	130	1	US-08-779-784-35
5	47	100.0	145	10	US-09-861-294-2
6	47	100.0	237	10	US-09-924-099-9
7	47	100.0	243	10	US-09-924-099-10
8	42	89.4	109	10	US-09-943-906-74
9	40	85.1	95	10	US-09-943-906-72
10	40	85.1	109	10	US-09-943-906-73
11	35	74.5	243	9	US-09-887-853-6
12	35	74.5	267	10	US-09-766-543-10
13	35	74.5	276	10	US-09-766-543-12
14	35	74.5	559	9	US-09-866-050A-499
15	34	72.3	107	8	US-08-844-215-12
16	34	72.3	108	9	US-09-848-798-178
17	34	72.3	405	10	US-09-864-761-38102
18	33	70.2	121	9	US-09-797-941A-4
19	33	70.2	245	9	US-09-797-941A-6
					Sequence 10, Appl
					Sequence 5, Appl
					Sequence 1, Appl
					Sequence 35, Appl
					Sequence 2, Appl
					Sequence 9, Appl
					Sequence 10, Appl
					Sequence 74, Appl
					Sequence 72, Appl
					Sequence 73, Appl
					Sequence 6, Appl
					Sequence 10, Appl
					Sequence 12, Appl
					Sequence 49, Appl
					Sequence 129, Appl
					Sequence 12, Appl
					Sequence 178, Appl
					Sequence 38102, A
					Sequence 4, Appl
					Sequence 6, Appl

20	33	70.2	303	9	US-09-510-332-125	Sequence 125, Appl
21	32	68.1	23	9	US-09-795-515-9	Sequence 9, Appl
22	32	68.1	107	9	US-09-999-025-15	Sequence 15, Appl
23	32	68.1	107	9	US-09-998-040-15	Sequence 15, Appl
24	32	68.1	107	9	US-09-998-817-15	Sequence 15, Appl
25	32	68.1	107	9	US-09-999-021-15	Sequence 15, Appl
26	32	68.1	107	9	US-10-040-997-15	Sequence 15, Appl
27	32	68.1	107	10	US-09-253-794-6	Sequence 6, Appl
28	32	68.1	108	10	US-09-229-200A-14	Sequence 14, Appl
29	32	68.1	569	10	US-09-765-272-154	Sequence 154, Appl
30	32	68.1	591	10	US-09-765-272-74	Sequence 74, Appl
31	31	66.0	88	9	US-09-862-540-41	Sequence 41, Appl
32	31	66.0	107	9	US-09-874-141-1	Sequence 1, Appl
33	31	66.0	107	9	US-09-874-141-2	Sequence 2, Appl
34	31	66.0	107	9	US-09-874-141-3	Sequence 3, Appl
35	31	66.0	107	9	US-09-874-141-4	Sequence 4, Appl
36	31	66.0	107	9	US-09-874-141-9	Sequence 9, Appl
37	31	66.0	111	10	US-09-920-171-7	Sequence 7, Appl
38	31	66.0	133	9	US-09-874-141-45	Sequence 45, Appl
39	31	66.0	133	9	US-09-874-141-47	Sequence 47, Appl
40	31	66.0	133	9	US-09-874-141-51	Sequence 51, Appl
41	31	66.0	150	9	US-09-782-397-5	Sequence 5, Appl
42	31	66.0	287	9	US-09-782-397-17	Sequence 17, Appl
43	31	66.0	304	9	US-09-782-397-14	Sequence 14, Appl
44	31	66.0	352	10	US-09-912-020-293	Sequence 293, Appl
45	31	66.0	2310	10	US-09-995-542-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-861-294-10
; Sequence 10, Application US/09861294
; Patent No.: US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-294-10

Query Match 100.0%; Score 47; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
Db 1 LOYASSPYT 9
| | | | | | | | | |

RESULT 2
US-09-924-099-5
; Sequence 5, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi

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; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-5

Query Match          100.0%; Score 47; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
Db 1 LOYASSPYT 9

RESULT 3
US-09-924-099-1
; Sequence 1, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-1

Query Match          100.0%; Score 47; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
Db 89 LOYASSPYT 97

RESULT 4
US-08-779-784-35
; Sequence 35, Application US/08779784
; Patent No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-35

Query Match          100.0%; Score 47; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
Db 111 LOYASSPYT 119

RESULT 5
US-09-861-294-2
; Sequence 2, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-09-861-294-2

Query Match 100.0%; Score 47; DB 10; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | | | |
DB 109 LOYASSPYT 117

RESULT 6

US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1

; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22

; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scfv) which neutralizes IL-18
US-09-924-099-9

Query Match 100.0%; Score 47; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | | | |
DB 219 LOYASSPYT 227

RESULT 7

US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1

; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33

;
; SEQ ID NO. 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scfv) which neutralizes IL-18
US-09-924-099-10

Query Match 100.0%; Score 47; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | | | |
DB 219 LOYASSPYT 227

RESULT 8

US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1

; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.,
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match 89.4%; Score 42; DB 10; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
| | | | | | | | | |
DB 89 LOYASSPYT 97

RESULT 9
US-09-943-906-72
; Sequence 72, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-943-906-72
Query Match 85.1%; Score 40; DB 10; Length 95;
Best Local Similarity 77.8%; Pred. No. 0.76;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOYASSPVT 9
| | | | | | | |
Db 75 LOYASSPFT 83
RESULT 10
US-09-943-906-73
; Sequence 73, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA

; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-943-906-73
Query Match 85.1%; Score 40; DB 10; Length 109;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOYASSPVT 9
| | | | | | | |
Db 89 LOYASSPFT 97
RESULT 11
US-09-887-853-6
; Sequence 6, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; Oppermann, Hermann
; Houston, L. L.
; Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-887-853-6

Query Match 74.5%; Score 35; DB 9; Length 243;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9
|||||
Db 222 LQYAIFFPT 230

RESULT 12

US-09-766-543-10
; Sequence 10, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 520C9
; OTHER INFORMATION: humanized single-chain antibody used in the
; OTHER INFORMATION: IL-2-antibody fusions
US-09-766-543-10

Query Match 74.5%; Score 35; DB 10; Length 267;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9
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Db 241 LQYAIFFPT 249

RESULT 13

US-09-766-543-12
; Sequence 12, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20

; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H520C9sFv plus
; OTHER INFORMATION: linker
US-09-766-543-12

Query Match 74.5%; Score 35; DB 10; Length 276;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9
|||||
Db 241 LQYAIFFPT 249

RESULT 14

US-09-866-050A-499
; Sequence 499, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011CAU
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 499
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Rat
US-09-866-050A-499

Query Match 74.5%; Score 35; DB 9; Length 559;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9
|||||
Db 325 LQNASAPYT 333

RESULT 15

US-08-844-215-12
; Sequence 12, Application US/08844215
; Patent No. US20020016445A1
; GENERAL INFORMATION:
; APPLICANT: PERSSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,215
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/635,109
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 80146.002
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-844-215-12

Query Match 72.3%; Score 34; DB 8; Length 107;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 90 QYGSPPYT 97

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Search completed: March 10, 2003, 17:11:28
Job time : 7.2931 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 : Search time 31.1034 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	21	AA1980
2	54	100.0	108	21	AA1981
3	54	100.0	135	21	AA1982
4	54	100.0	237	21	AA1983
5	54	100.0	243	21	AA1984
6	42	77.8	90	16	AA1985
7	42	77.8	92	20	AA1986
8	42	77.8	92	20	AA1987
9	42	77.8	107	16	AA1988
10	42	77.8	107	16	AA1989

11	42	77.8	107	16	AA1990	Light chain variab
12	42	77.8	107	18	AA27121	Murine antibody li
13	42	77.8	108	13	AA21310	Light chain of Mf
14	42	77.8	109	18	AA18271	Prp 37 light chain
15	42	77.8	109	20	AAW85910	Prp 37 light chain
16	42	77.8	109	22	AA66862	Anti-Prp antibody
17	42	77.8	109	23	ABP51796	Anti-prion protein
18	42	77.8	252	23	AAU72863	P4-14 single chain
19	42	77.8	257	23	AAU72869	P5-11 single chain
20	42	77.8	499	23	AAU72872	3B10xP4-14 bispec
21	41	75.9	109	20	AA106388	Humanised LM609 an
22	41	75.9	109	20	AA106382	Humanised LM609 an
23	39	72.2	107	21	AA190824	520C9 hybridoma VL
24	39	72.2	112	23	AAW50879	Anti-bovine prion
25	39	72.2	243	17	AAW02280	520C9 anti-c-erbB-
26	39	72.2	243	19	AAW53170	520C9 anti-c-erbB-
27	39	72.2	243	20	AAW80424	520C9 sfv sequence
28	39	72.2	246	14	AA195569	Sequence of 520C9
29	39	72.2	267	22	AAU04944	Humanised anti-p18
30	39	72.2	409	22	AAU04945	Humanised anti-p18
31	39	72.2	534	14	AA195711	Sequence of G-FIT
32	38	70.4	11	23	AB177068	AC2885 antibody li
33	38	70.4	88	21	AA156653	Partial peptide fr
34	38	70.4	95	18	AA18269	Prp 81 light chain
35	38	70.4	95	20	AAW85908	Prp 81 light chain
36	38	70.4	95	22	AA658860	Anti-Prp antibody
37	38	70.4	95	23	ABP51794	Anti-prion protein
38	38	70.4	109	18	AA18270	Prp 28 light chain
39	38	70.4	109	20	AAW85909	Prp 28 light chain
40	38	70.4	109	22	AA668661	Anti-Prp antibody
41	38	70.4	109	23	ABP51795	Anti-prion protein
42	38	70.4	126	23	AB177064	AC2885 antibody li
43	38	70.4	128	21	AA156718	Amino acid sequenc
44	38	70.4	145	18	AAW27119	Murine monoclonal
45	38	70.4	145	20	AAW87593	Antibody 11D10 lig

ALIGNMENTS

RESULT 1
AA1980
ID AAY44589 standard; Protein; 11 AA.
AC AAY44589;
DT 04-APR-2000 (first entry)
DE Mouse anti-IL-18 antibody VL complementarity-determining region-1.
KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW complementarity-determining region; CDR; hybridoma #125-2H; mouse;
KW monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;
KW immunosuppressive; leucocytopenic; antiallgic; antipyretic;
KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
KW inflammatory disorder; immunoreaction.
XX Mus musculus.
XX EP974600-A2.
XX 26-JAN-2000.
XX 24-JUN-1999; 99EP-0304977.
XX 24-JUN-1998; 98JP-0177580.
XX 12-OCT-1998; 98JP-0289044.
XX 22-DEC-1998; 98JP-0365023.
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX

DR WPI; 2000-118341/11.
 DR N-PSDB; AAZ49536.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Claim 7; Page 18; 36pp; English.
 XX
 CC The present protein sequence is a complementarity-determining region
 CC (CDR) of mouse anti-Interleukin-18 antibody light chain variable region
 CC (VL) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
 CC sequence can be used in the production of recombinant monoclonal antibody
 CC #125-2HmAb, which is capable of neutralising biological activities of
 CC interleukin-18. The antibody has anti-inflammatory, immunosuppressive,
 CC leucocytopenic, antiallgic, antipyretic, antiallergic and hepatotropic
 CC activity and can be used for prevention and treatment of autoimmune
 CC diseases, immunopathies and inflammatory disorders caused by excessive
 CC immunoreaction.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 54; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQDIGSKLY 11
 Db 1 RASQDIGSKLY 11
 RESULT 2
 AAY44587
 ID AAY44587 standard; Protein; 108 AA.
 AC
 XX AAY44587;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse anti-IL-18 antibody light chain variable region.
 KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
 KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
 KW antiinflammatory; immunosuppressive; leucocytopenic; antiallgic;
 KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
 KW immunopathy; inflammatory disorder; immunoreaction.
 XX
 OS Mus musculus.
 XX
 PN EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 PF 24-JUN-1999; 99EP-0304977.
 XX
 PR 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX
 DR WPI; 2000-118341/11.
 DR N-PSDB; AAZ49534.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Claim 5; Page 17; 36pp; English.
 XX
 CC The present protein sequence is the mouse anti-Interleukin-18 antibody

CC light chain variable region (VL) encoded by cDNA derived from hybridoma
 CC #125-2H. The nucleotide sequence is used in the production of recombinant
 CC monoclonal antibody #125-2HmAb, which is capable of neutralising
 CC biological activities of interleukin-18. The antibody has antiallgic,
 CC antiinflammatory, immunosuppressive, leucocytopenic, antipyretic,
 CC antiallergic and hepatotropic activity and can be used for prevention and
 CC treatment of autoimmune diseases, immunopathies and inflammatory
 CC disorders caused by excessive immunoreaction.
 XX
 SQ Sequence 108 AA;
 Query Match 100.0%; Score 54; DB 21; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQDIGSKLY 11
 Db 24 RASQDIGSKLY 34
 RESULT 3
 AAY44599
 ID AAY44599 standard; Protein; 135 AA.
 XX
 AC AAY44599;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse light chain variable region encoded by PCR A product.
 XX
 KW Mouse light chain variable region; VL; variable region light chain;
 KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
 KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
 KW hematopoietic; leukocytopenic; antiallgic; antipyretic.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PN EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 PF 24-JUN-1999; 99EP-0304977.
 XX
 PR 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX
 DR WPI; 2000-118341/11.
 DR N-PSDB; AAZ49548.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Disclosure; Page 28-29; 32pp; English.
 XX
 CC The present sequence is the mouse light chain variable region. This was
 CC encoded by a recombinant DNA is derived from PCR A which amplifies
 CC antibody light chain variable region (VL). The transformant produced
 CC using the VL gene was used transform competent E. coli cells. The peptide
 CC produced by transformants neutralises interleukin-18. This is useful for
 CC treating and preventing immunopathies, inflammatory disorders and
 CC autoimmune diseases which are caused by excessive immunoreaction. The
 CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
 CC hematopoietic, leukocytopenic, antiallgic, antipyretic and hepatic
 CC -function improving activities.
 XX
 SQ Sequence 135 AA;

Query Match 100.0%; Score 54; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQDIGSKLY 11
DB 44 RASQDIGSKLY 54

RESULT 4

AA444595
ID AAY44595 standard; Protein; 237 AA.

XX AC AAY44595;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H recombinant protein.

XX KW EscFv#125-2H recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX OS Mus musculus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113 /note= "Heavy chain variable region"

FT Domain 114..130 /note= "Glycine-serine linker"

FT Domain 131..237 /note= "Light chain variable region"

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Query Match 100.0%; Score 54; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASQDIGSKLY 11
DB 44 RASQDIGSKLY 54

RESULT 4

AA444595
ID AAY44595 standard; Protein; 237 AA.

XX AC AAY44595;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H recombinant protein.

XX KW EscFv#125-2H recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX OS Mus musculus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113 /note= "Heavy chain variable region"

FT Domain 114..130 /note= "Glycine-serine linker"

FT Domain 131..237 /note= "Light chain variable region"

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OY 1 RASQDIGSKLY 11
DB 154 RASQDIGSKLY 164

RESULT 5

AA444596

ID AAY44596 standard; Protein; 243 AA.

XX AC AAY44596;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H.HT recombinant protein.

XX KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX OS Mus musculus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113 /note= "Heavy chain variable region"

FT Domain 114..130 /note= "Glycine-serine linker"

FT Domain 131..237 /note= "Light chain variable region"

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OY 1 RASQDIGSKLY 11
DB 154 RASQDIGSKLY 164

RESULT 5

AA444596

ID AAY44596 standard; Protein; 243 AA.

XX AC AAY44596;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H.HT recombinant protein.

XX KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX OS Mus musculus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113 /note= "Heavy chain variable region"

FT Domain 114..130 /note= "Glycine-serine linker"

FT Domain 131..237 /note= "Light chain variable region"

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OY 1 RASQDIGSKLY 11
DB 154 RASQDIGSKLY 164

RESULT 5

AA444596

ID AAY44596 standard; Protein; 243 AA.

XX AC AAY44596;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H.HT recombinant protein.

XX KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX OS Mus musculus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113 /note= "Heavy chain variable region"

FT Domain 114..130 /note= "Glycine-serine linker"

FT Domain 131..237 /note= "Light chain variable region"

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OY 1 RASQDIGSKLY 11
DB 154 RASQDIGSKLY 164

RESULT 5

AA444596

ID AAY44596 standard; Protein; 243 AA.

XX AC AAY44596;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H.HT recombinant protein.

XX KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

XX OS Mus musculus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113 /note= "Heavy chain variable region"

FT Domain 114..130 /note= "Glycine-serine linker"

FT Domain 131..237 /note= "Light chain variable region"

FT FT

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Db 154 RASQDIGSKLY 164
|||||

RESULT 6
AAR80078
ID AAR80078 standard; Protein; 90 AA.

XX AAR80078;

XX 22-MAY-1996 (first entry)

XX Mouse derived light chain RT3 phage antibody pattern A.

XX Light chain; RT3; murine; catalytic antibody; bacteriophage;
pattern A.

XX Mus musculus.

XX Key Location/Qualifiers
FT Region 1..15
FT /note= "framework region 1"
FT Region 16..26
FT /note= "complementarity determining region 1"
FT Region 27..40
FT /note= "framework region 2"
FT Region 41..47
FT /note= "complementarity determining region 2"
FT Region 48..78
FT /note= "framework region 3"
FT Region 79..88
FT /note= "complementarity determining region 3"
FT Region 89..90
FT /note= "framework region 4
FT N-terminal fragment"

XX WO9527045-A1.

XX 12-OCT-1995.

XX 30-MAR-1994; 94WO-US03420.

XX 30-MAR-1994; 94WO-US03420.

XX (IGEN-) IGEN INC.

XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;

XX WPI; 1995-358624/46.

XX N-PSDB; AAT04625.

XX Production of catalytic antibodies displayed on phage - by
generating a gene library of antibody-derived domains and expressing
it in phage vectors

XX Disclosure; Fig 9; 133pp; English.

XX AAT04625 encodes AAR80078 mouse derived light chain RT3 phage antibody.
The DNA was used in the prepn. of catalytic antibody (CA) producing
bacteriophage. The CAs can be used to activate/deactivate a
biological function in an animal by enhancing the rate of cleavage,
or formation of a specific bond within a mol. in vivo.

XX Sequence 90 AA;

Query Match 77.8%; Score 42; DB 16; Length 90;
Best Local Similarity 90.8%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10

Db 16 RASQDIGSSL 25

RESULT 7

AAW95480

ID AAW95480 standard; Protein; 92 AA.

XX AAW95480;

XX 29-MAR-1999 (first entry)

XX Mouse derived RT3 phage antibody light chain pattern C genetic sequence.

XX Catalytic; antibody; phage display; immunising; phage expression vector;
prodrug; scFv.

XX Mus sp.

XX US5855885-A.

XX 05-JAN-1999.

XX 14-JUL-1994; 94US-0273146.

XX 22-JAN-1993; 93US-0007684.

XX 14-JUL-1994; 94US-0273146.

XX (CHIS/) CHISWELL D.

XX (DARS/) DARSLEY M J.

XX (FITZ/) FITZGERALD K.

XX (KENT/) KENTEN J H.

XX (MART/) MARTIN M T.

XX (MCCA/) MCCAFFERTY J.

XX (SMIT/) SMITH R.

XX (TITM/) TITMAS R C.

XX (WILL/) WILLIAMS R O.

XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

XX Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;

XX WPI; 1999-105036/09.

XX N-PSDB; AAX00879.

XX Production of catalytic antibodies displayed on bacteriophages -
comprises generating a gene library of antibody-derived domains
inserting coding into a phage expression vector and isolating the
catalytic antibodies

XX Example 4; Fig 11; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies
displayed on a phage. The method comprises: (a) generating a gene library
of antibody-derived domains; (b) inserting coding for the domains into a
phage expression vector; and (c) isolating the catalytic antibodies. The
phage expression vector incorporates a histidine peptide in tandem with a
myc peptide. The catalytic antibodies can be isolated by preparing an
antigen; optionally immunising an animal with the antigen; generating a
library of VH and VL domains from the immunised animal; cloning the VH
and VL domains into a phage expression vector to generate phage display
antibodies; selecting phage display antibodies which bind specifically
to the antigen; screening the selected phage display antibodies for
catalytic activity to substrate; and isolating the catalytic antibodies,
where the phage expression vector incorporates a histidine peptide in
tandem with a myc peptide. The processes are used to produce catalytic
antibodies, which can be used for in vivo activation of a prodrug. The
present sequence represents a genetic sequence of light chain PCR
pattern C from mouse derived RT3 phage antibodies.

XX Sequence 92 AA;

Query Match 77.8%; Score 42; DB 20; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASODIGSKL 10
 Db 16 RASODIGSSL 25

RESULT 8

AAW95476
 ID AAW95476 standard; Protein; 92 AA.

XX AAW95476;

DT 29-MAR-1999 (first entry)

XX Mouse derived RT3 phase antibody light chain pattern A genetic sequence.

XX Catalytic; antibody; phage display; immunising; phage expression vector;
 produg; scfv.

XX Mus sp.

XX US5855885-A.

XX 05-JAN-1999.

XX 14-JUL-1994; 94US-0273146.

XX 22-JAN-1993; 93US-0007684.

XX 14-JUL-1994; 94US-0273146.

XX (CHIS/) CHISWELL D.

XX (DARS/) DARSLEY M J.

XX (FITZ/) FITZGERALD K.

XX (KENT/) KENTEN J H.

XX (MART/) MARTIN M T.

XX (MCCA/) MCCAFFERTY J.

XX (SMIT/) SMITH R.

XX (TITM/) TITMAS R C.

XX (WILL/) WILLIAMS R O.

XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;

XX WPI: 1999-105036/09.

XX N-PSDB: AAX00875.

XX Production of catalytic antibodies displayed on bacteriophages -
 PT comprises generating a gene library of antibody-derived domains
 PT inserting coding into a phage expression vector and isolating the
 PT catalytic antibodies

XX Example 4; Fig 9A-F; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies
 CC displayed on a phage. The method comprises: (a) generating a gene library
 CC of antibody-derived domains; and (b) inserting coding for the domains into a
 CC phage expression vector; and (c) isolating the catalytic antibodies. The
 CC phage expression vector incorporates a histidine peptide in tandem with a
 CC myc peptide. The catalytic antibodies can be isolated by preparing an
 CC antigen; optionally immunising an animal with the antigen; generating a
 CC library of VH and VL domains from the immunised animal; cloning the VH
 CC and VL domains into a phage expression vector to generate phage display
 CC antibodies; selecting phage display antibodies which bind specifically
 CC to the antigen; screening the selected phage display antibodies for
 CC catalytic activity to substrate; and isolating the catalytic antibodies,
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug. The
 CC present sequence represents a genetic sequence of light chain pattern A
 CC from mouse derived RT3 phage antibodies.

XX Sequence 92 AA;

SQ Query Match

77.8%; Score 42; DB 20; Length 92;

Best Local Similarity 90.0%; Pred. No. 0.89;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASODIGSKL 10
 Db 16 RASODIGSSL 25

RESULT 9

AAW78972
 ID AAR78972 standard; Protein; 107 AA.

XX AAR78972;

DT 21-DEC-1995 (first entry)

XX Light chain variable region for monoclonal antibody 5B6.

XX Monoclonal antibody; heavy metal; mercury; variable region;
 KW light chain.

XX Synthetic.

XX WO9520607-A.

XX 03-AUG-1995.

XX 27-JAN-1995; 95WO-US01199.

XX 27-JAN-1994; 94US-0187407.

XX (BTON-) BIONEBRASKA INC.

XX Lopez O, Wagner FW, Wylie DE;

XX WPI: 1995-275415/36.

XX N-PSDB: AAQ97510.

XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals

XX Claim 23; Page 70; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of
 CC BALB/c mouse that had received multiple injections of mercuric ions
 CC reacted with glutathione to produce a mercuric ion coordinate
 CC covalent compound which was covalently bound to keyhole limpet
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
 CC 5B6 and 3E8) were producing MABs that were strongly positive
 CC against glutathione-mercuric ions but negative against glutathione
 CC without mercuric ions. RNA was isolated from hybridoma cells with
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
 CC by Muv reverse transcriptase. The primers used for cDNA synthesis
 CC were complementary to the 5' end of the CHI domain of the heavy
 CC chain expressed by the hybridoma of interest, or to the 5' and of
 CC the C kappa domain. Some of the primers used for cDNA synthesis are
 CC shown in AAQ97511-097518. The primer used for cDNA synthesis of the
 CC variable region of a particular antibody polypeptide was also used
 CC for PCR amplification of that variable region, in conjunction with
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518
 CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
 CC of the PCR amplified nucleotides were determined. These are given
 CC in AAQ97498-097510 and the deduced AA sequences in AAR79241-R79250 &
 CC AAR78970-R78971. The descriptions of the SPQ ID nos given on pp 44-45
 CC and in the claims are different from the descriptions in the
 CC sequence listings. The descriptions in the sequence listings are
 CC used here.

XX Sequence 107 AA;

SQ Query Match

77.8%; Score 42; DB 16; Length 107;

Best Local Similarity 90.0%; Pred. No. 1;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 10

AAR79247
ID AAR79247 standard; Protein; 107 AA.

XX AAR79247;
AC AAR79247;

XX 21-DEC-1995 (first entry)
DT

XX Light chain variable region for monoclonal antibody 1F10.
DE

XX Monoclonal antibody; heavy metal; mercury; variable region;
DE

KW light chain.
KW

XX Synthetic.
XX

XX WO9520607-A.
PN

XX 03-AUG-1995.
PD

XX 27-JAN-1995; 95WO-US01199.
PF

XX 27-JAN-1994; 94US-0187407.
PR

XX (BION-) BIONEBRASKA INC.
PA

XX Lopez O, Wagner FW, Wylie DE;
PI

XX WPI: 1995-275415/36.
DR

XX N-PSDB; AAQ97504.
DR

XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
PT

XX Claim 23; Page 62; 106pp; English.
PS

XX Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MABs that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the MAB 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
CC

XX Sequence 107 AA;
SQ

Query Match 77.8%; Score 42; DB 16; Length 107;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
| | | | | | | | | |
Db 24 RASQDIGSSL 33

RESULT 11

AAR79250
ID AAR79250 standard; Protein; 107 AA.

XX AAR79250;
AC AAR79250;

XX 21-DEC-1995 (first entry)
DT

XX Light chain variable region for monoclonal antibody 5G4.
DE

XX Monoclonal antibody; heavy metal; mercury; variable region;
DE

KW light chain.
KW

XX Synthetic.
XX

XX WO9520607-A.
PN

XX 03-AUG-1995.
PD

XX 27-JAN-1995; 95WO-US01199.
PF

XX 27-JAN-1994; 94US-0187407.
PR

XX (BION-) BIONEBRASKA INC.
PA

XX Lopez O, Wagner FW, Wylie DE;
PI

XX WPI: 1995-275415/36.
DR

XX N-PSDB; AAQ97507.
DR

XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
PT

XX Claim 23; Page 66; 106pp; English.
PS

XX Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MABs that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the MAB 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
CC

XX Sequence 107 AA;
SQ

Query Match 77.8%; Score 42; DB 16; Length 107;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASQDIGSKL 10
 Db 24 RASQDIGSSL 33

RESULT 12

AAW27121
 ID AAW27121 standard; Protein; 107 AA.

XX AC AAW27121;
 XX DT 04-JAN-1998 (first entry)

XX DE Murine antibody light chain variable region consensus.
 XX KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
 KW human milk fat globule; HMEG; tumour; breast cancer; vaccine.
 XX OS Mus musculus.

XX FH Key Location/Qualifiers
 FT Region 24..34
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50..56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 88..96
 FT /label= CDR3
 FT /note= "complementarity determining region 3"

XX PN W09722699-A2.
 XX PD 26-JUN-1997.
 XX PE 19-DEC-1996; 96WO-US20757.
 XX PR 13-DEC-1996; 96US-0575762.
 XX PR 20-DEC-1995; 95US-0575762.
 XX PR 26-JAN-1996; 96US-0591965.
 XX PA (KENT) UNIV KENTUCKY.

XX PI Chatterjee M, Chatterjee SK, Foon KA;
 XX DR WPI; 1997-341690/31.

XX PT Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer

XX PS Example 2; Fig 26C; 130pp; English.

XX CC This polypeptide sequence comprises a consensus sequence of murine
 CC light chain variable regions (VL) selected on the basis of identity
 CC to the VL region (see W271119) of monoclonal anti-idiotypic antibody
 CC 11D10. The sequences were obtained from a GenBank database
 CC search. A VH consensus (W27122) was also produced. 11D10 has at
 CC least 18 departures from the consensus sequences (7 in the light
 CC chain and 11 in the heavy chain). 8 occur within CDRs and 10
 CC outside CDRs. 11D10 polypeptides and polynucleotides can be
 CC used in vaccines and pharmaceutical compositions for the treatment
 CC of human milk fat globule-associated diseases such as breast
 CC cancer.

XX SQ Sequence 107 AA;
 Query Match 77.8%; Score 42; DB 18; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASQDIGSKL 10
 Db 24 RASQDIGSSL 33

RESULT 13

AAR21310
 ID AAR21310 standard; Protein; 108 AA.

XX AC AAR21310;
 XX DT 21-MAY-1992 (first entry)

XX DE Light chain of M1f clone.
 XX KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
 KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Region 25..34
 FT /label= CDR1
 FT Region 50..56
 FT /label= CDR2
 FT Region 89..96
 FT /label= CDR3

XX PN W09201047-A.
 XX PD 23-JAN-1992.

XX PF 10-JUL-1991; 91WO-GB01134.
 XX PR 15-MAY-1991; 91GB-0010549.
 XX PR 10-JUL-1990; 90GB-0015198.
 XX PR 19-OCT-1990; 90GB-0022845.
 XX PR 12-NOV-1990; 90GB-0024503.
 XX PR 06-MAR-1991; 91GB-0004744.

XX PA (CAMP-) CAMBRIDGE ANTIBODY.
 PA (MEDI-) MED RES COUNCIL.

XX PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
 PI Winter GP, Bonnett TP;
 XX DR WPI; 1992-056862/07.

XX PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.

XX PS Example 46; Fig 52; 109pp; English.

XX CC The sequence is the light chain of clone M1f encoding an scFv frag-
 CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).
 CC The DNA encoding the chain was amplified from a cDNA library prepd.
 CC from the spleen of an unimmunised mouse. The corresponding heavy
 CC chain was also amplified from an existing construct, pSWI-VHpl.3
 CC (Ward et al, 1989). The two fragments were assembled via a linker
 CC to prepare an scFv construct which was ligated into the fdCAT2
 CC vector for expression on the surface of fd bacteriophage. In this
 CC way, the VL domain was replaced by a library of VL domains to allow
 CC for selection of a broader range of antibody specificities. Several
 CC clones were isolated which bound to TEL (the parent antibody D1.3
 CC binds exclusively to HEL). The sequences of the light chains of
 CC two of these clones, MFI and M21 are given in AAR21310 and AAR21311
 CC respectively. The D1.3 light chain is given in AAR21309.
 CC See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.

XX SQ Sequence 108 AA;
 Query Match 77.8%; Score 42; DB 13; Length 108;

Best Local Similarity 90.0%; Pred. No. 1.1; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 24 RASQDIGSSL 33

RESULT 14
AAW18271
ID AAW18271 standard; peptide; 109 AA.
AC AAW18271;
XX
DT 09-JAN-1998 (first entry)
XX
DE PrP 37 light chain variable region.
XX
KW Prion protein; Prp; heavy chain variable region; antibody; scrapie; light chain variable region; PrP-Sc; pathogen; fatal familial insomnia; central nervous system spongiform encephalopathy; human; therapy; transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease; bovine spongiform encephalopathy; feline spongiform encephalopathy; Serstmann-Strassler-Scheinker Disease.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1..23
FT /note= "framework region 1"
FT Region 24..34
FT /note= "complementarity determining region 1"
FT Region 35..49
FT /note= "framework region 2"
FT Region 50..56
FT /note= "complementarity determining region 2"
FT Region 57..88
FT /note= "framework region 3"
FT Region 89..97
FT /note= "complementarity determining region 3"
FT Region 98..109
FT /note= "framework region 4"
XX
PN W09710505-A1.
XX
PD 20-MAR-1997.
XX
PF 13-SEP-1996; 96WO-US14840.
XX
PR 14-SEP-1995; 95US-0528104.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Burton DR, Prusiner SB, Williamson RA;
XX WPI; 1997-202357/18.
XX
PT New antibodies to the scrapie isoform of prion protein - used for detection of infectious prion proteins or for treating disease such as BSE, CJD or scrapie
XX
PS Example 9; Fig 6; 99pp; English.
XX
CC AAW18266-W18285 represent portions of the antibodies of the invention. The antibodies of the invention are able to bind the scrapie isoform of prion protein PrP-Sc in situ. Prions are infectious pathogens that cause central nervous system spongiform encephalopathies in humans and animals. The scrapie isoform of the prion protein (PrP-Sc) is necessary for both the transmission and pathogenesis of the transmissible neurodegenerative diseases of animals and humans. The antibodies can be used in a method of the invention for detecting human PrP-Sc in a source. The antibodies specifically bind to prion proteins associated with disease and do not bind to denatured PrP proteins not associated with

CC disease. They can bind to prion proteins of a specific species of mammals. They can also have the ability to neutralise infectious prions. The antibodies can be used for screening for the presence of prions in products such as pharmaceuticals, food or cosmetics. They can also be used for prion neutralisation to purify products, for extraction of prion proteins or for therapy, for diseases such as bovine spongiform encephalopathy, Creutzfeldt-Jakob Disease, fatal familial insomnia or Serstmann-Strassler-Scheinker Disease, scrapie or feline spongiform encephalopathies.
XX
SQ Sequence 109 AA;

Query Match 77.8%; Score 42; DB 18; Length 109;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
Db 24 RASQDIGSSL 33

RESULT 15
AAW85910
ID AAW85910 standard; peptide; 109 AA.
XX
AC AAW85910;
XX
DT 12-FEB-1999 (first entry)
XX
DE PrP 37 light chain variable region.
XX
KW PrP; PrP(Sc); scrapie; isoform; antibody; prion; CJD; screening; Creutzfeldt-Jakob disease; infectivity; assay; pharmaceutical; food; cosmetic; therapeutic; mouse.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 1..23
FT /note= "Framework 1"
FT Region 24..34
FT /note= "complementarity determining region 1 (CDR1)"
FT Region 35..49
FT /note= "Framework 2"
FT Region 50..56
FT /note= "complementarity determining region 2 (CDR2)"
FT Region 57..88
FT /note= "Framework 3"
FT Region 89..97
FT /note= "complementarity determining region 3 (CDR3)"
FT Region 98..109
FT /note= "Framework 4"
XX
PN US5846533-A.
XX
PD 08-DEC-1998.
XX
PF 13-SEP-1996; 96US-0713939.
XX
PR 13-SEP-1996; 96US-0713939.
PR 14-SEP-1995; 95US-0528104.
XX
PA (SCRI) SCRIPPS RES INST.
XX (REGC) UNIV CALIFORNIA.
XX
PI Burton DR, Prusiner SB, Williamson RA;
XX WPI; 1999-058996/05.
XX
PT Antibody specific for scrapie isoform of prion protein - useful for diagnosis and therapy
XX
PS Example 9; Fig 6A-B; 58pp; English.

XX The invention relates to an antibody that is capable of binding to
 CC native PrP(Sc), the scrapie isoform of prion protein (PrP). The antibody
 CC is produced by a method that comprises synthesising a library of
 CC antibodies on phages, contacting the phages with a composition containing
 CC PrP proteins, isolating phages that bind to native PrP(Sc) in situ,
 CC obtaining an antibody from the phages, and optionally analysing the
 CC phages to determine a nucleic acid sequence encoding an amino acid
 CC sequence to which the native PrP(Sc) binds. The antibody is used to
 CC detect disease- associated PrP, especially in Creutzfeldt-Jakob disease
 CC (CJD) and distinguish it from normal PrP. They can also be used to
 CC neutralise the infectivity of PrP(Sc). Assays using the antibodies can be
 CC used to screen for disease-associated PrP in pharmaceutical products,
 CC cosmetics and foods or for therapeutic purposes. Sequences AAW85908 to
 CC AAW85910 represent light chain variable regions of the phage clones
 CC generated by panning an IgG1 library from mouse D7282 against denatured
 CC PrP.

XX SQ Sequence 109 AA;

Query Match 77.8%; Score 42; DB 20; Length 109;
 Best Local Similarity 90.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASQDIGSKL 10
 Db 24 RASQDIGSSL 33

Search completed: March 10, 2003, 16:56:55
 Job time : 32.1034 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 19.7931 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	AAW70945	CDR2 of the light
2	31	100.0	7	AAV44587	Mouse anti-IL-18 a
3	31	100.0	90	AAW85910	Mouse derived lig
4	31	100.0	92	AAW95480	Mouse derived RT3
5	31	100.0	92	AAW95476	Mouse derived RT3
6	31	100.0	95	AAW70954	Light chain of mon
7	31	100.0	97	ABP33764	Human transport pr
8	31	100.0	107	AAW27121	Murine antibody li
9	31	100.0	107	AAV90824	520C9 hybridoma VL
10	31	100.0	108	AAW21310	Light chain of Mf

11	31	100.0	108	AAV44587	Mouse anti-IL-18 a
12	31	100.0	109	AAW18271	Prp 37 light chain
13	31	100.0	109	AAW85910	Prp 37 light chain
14	31	100.0	109	AAW85862	Anti-Prp antibody
15	31	100.0	109	ABP51796	Anti-prion protein
16	31	100.0	112	AAW50879	Anti-bovine prion
17	31	100.0	135	AAV44599	Mouse light chain
18	31	100.0	146	AAV30251	Sequence of the le
19	31	100.0	147	AAW75566	Human colon cancer
20	31	100.0	237	AAV44595	Escfv#125-2H recom
21	31	100.0	243	AAW02280	520C9 anti-c-erbB-
22	31	100.0	243	AAW53170	520C9 anti-c-erbB-
23	31	100.0	243	AAW80424	520C9 svf sequence
24	31	100.0	243	AAV44596	Escfv#125-2H.Ht re
25	31	100.0	246	AAW39569	Sequence of 520C9
26	31	100.0	252	AAW72863	p4-14 single chain
27	31	100.0	257	AAW72869	p5-11 single chain
28	31	100.0	267	AAU04944	Humanised anti-pl8
29	31	100.0	409	AAU04945	Humanised anti-pl8
30	31	100.0	499	AAU72872	3B10P4-14 bispeci
31	31	100.0	555	AAW70797	S cerevisiae apopt
32	31	100.0	606	ABW57811	Drosophila melanog
33	31	100.0	606	ABW57812	Drosophila melanog
34	31	100.0	722	AAW29411	Human protein sequ
35	31	100.0	747	AAW89585	Human ATP-binding
36	31	100.0	747	AAW13355	Human ATP-binding
37	31	100.0	752	AAW14068	Human ABC-Transpor
38	29	93.5	1552	ABW71764	Drosophila melanog
39	29	93.5	1561	ABG22379	Novel human diago
40	29	93.5	1792	AAW39065	Human polypeptide
41	29	93.5	1870	ABG22378	Novel human diago
42	29	93.5	2447	ABG22380	Novel human diago
43	28	90.3	80	AAW52602	Helicobacter pylori
44	28	90.3	272	AAW20101	H. pylori transpor
45	28	90.3	285	AAW20861	H. pylori cell env

ALIGNMENTS

RESULT 1

AAW70945
ID AAW70945 standard; peptide: 7 AA.

XX AAW70945;

XX AC

XX AAW70945;

XX AC

XX AAW70945;

XX AC

XX AAW70945;

XX AC

XX AAW70945;

XX AC

XX AAW70945;

XX AC

XX AAW70945;

XX AC

XX AAW70945;

XX AC

XX AAW70945;

XX AC

DE CDR2 of the light chain of monoclonal antibody RS-255.

XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
XX respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
XX viral infection; inhibit; fusion; protection; transcription;
XX antiviral agent; prophylaxis; diagnosis; infection; contamination.

XX Synthetic.

XX OS

XX Mus sp.

XX FR2758331-A1.

XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-0000300.

XX 14-JAN-1997; 97FR-0000300.

XX (UYBO-) UNIV BOURGOGNE.

XX Bourgeois C, Kohli E, Pothier P;

XX WPI: 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa -

PT useful for, e.g. diagnosing, preventing and treating viral
infection(s)

XX Claim 12; Page 39; 51pp; French.

XX AAW70905-46 represent peptide sequences that can recognise, by
PS antigen-antibody type reactions, at least 1 epitope of a pathogenic
CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are
CC analogous to CDR regions of monoclonal antibodies specific for
CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR
CC regions of monoclonal antibodies specific for site III or IV of the
CC VP6 protein of rota virus (RV). The peptides can neutralise viral
CC infections and may also inhibit fusion between infected and uninfected
CC cells or cells and viruses. They provide passive or active protection
CC and/or inhibit transcription of the virus, so are useful as antiviral
CC agents or for prophylaxis, in human or veterinary medicine. The peptides
CC can be labelled and used to diagnose infection or contamination by the
CC virus. The peptides are particularly directed against RSV or RS but may
CC also be used against papilloma, adeno, entero, polio, influenza or
CC immune deficiency viruses.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||

DB 1 ATSSLDS 7

RESULT 2

AAAY44590
ID AAY44590 standard; Protein; 7 AA.

XX AC AAY44590;

XX DT 04-APR-2000 (first entry)

XX DE Mouse anti-IL-18 antibody VL complementarity-determining region-2.

XX KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW complementarity-determining region; CDR; hybridoma #125-2H; mouse;
KW monoclonal antibody #125-2HmAb; interleukin-18; antinflammatory;
KW immunosuppressive; leucocytopenic; antialgic; antipyretic;
KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
KW inflammatory disorder; immunoreaction.

XX OS Mus musculus.

XX PN EP974600-A2.

XX PD 26-JAN-2000.

XX PE 24-JUN-1999; 99EP-0304977.

XX PR 24-JUN-1998; 98JP-0177580.

XX PR 12-OCT-1998; 98JP-0289044.

XX PR 22-DEC-1998; 98JP-0365023.

XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX DR WPI; 2000-118341/11.

XX DR N-PSDB; AA249537.

XX PT New artificially produced peptide for neutralizing biological activity

XX PT of interleukin-18, useful for treating and preventing immunopathies,

XX PT inflammatory disorders and autoimmune diseases -

XX Claim 7; Page 18; 36pp; English.

PS

XX

CC The present protein sequence is a complementarity-determining region
CC (CDR) of mouse anti-Interleukin-18 antibody light chain variable region
CC (VL) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
CC sequence can be used in the production of recombinant monoclonal antibody
CC #125-2HmAb, which is capable of neutralising biological activities of
CC interleukin-18. The antibody has antinflammatory, immunosuppressive,
CC leucocytopenic, antialgic, antipyretic, antiallergic and hepatotropic
CC activity and can be used for prevention and treatment of autoimmune
CC diseases, immunopathies and inflammatory disorders caused by excessive
CC immunoreaction.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||

DB 1 ATSSLDS 7

RESULT 3

AAR80078

ID AAR80078 standard; Protein; 90 AA.

XX AC AAR80078;

XX DT 22-MAY-1996 (first entry)

XX DE Mouse derived light chain RT3 phase antibody pattern A.

XX KW Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW pattern A.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Region 1..15 /note= "framework region 1"

FT Region 16..26 /note= "complementarity determining region 1"

FT Region 27..40 /note= "framework region 2"

FT Region 41..47 /note= "complementarity determining region 2"

FT Region 48..78 /note= "framework region 3"

FT Region 79..88 /note= "complementarity determining region 3"

FT Region 89..90 /note= "framework region 4"

FT Region /note= "N-terminal fragment"

XX PN WO9527045-A1.

XX PD 12-OCT-1995.

XX PF 30-MAR-1994; 94WO-US03420.

XX PR 30-MAR-1994; 94WO-US03420.

XX PA (IGEN-) IGEN INC.

XX PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

XX PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;

XX DR WPI; 1995-358624/46.

XX DR N-PSDB; AAT04625.

XX PT Production of catalytic antibodies displayed on phage - by

XX PT generating a gene library of antibody-derived domains and expressing

PT it in phage vectors

XX Disclosure; Fig 9; 133pp; English.

CC AAT04625 encodes AAR80078 mouse derived light chain RT3 phage antibody.
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing
 CC bacteriophage. The CA can be used to activate/deactivate a
 CC biological function in an animal by enhancing the rate of cleavage,
 CC or formation of a specific bond within a mol. in vivo.

XX Sequence 90 AA;

Query Match 100.0%; Score 31; DB 16; Length 90;

Best Local Similarity 100.0%; Pred. No. 9.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

Db 41 ATSSLS 47

RESULT 4

AAW95480

ID AAW95480 standard; Protein; 92 AA.

XX AC AAW95480;

XX DT 29-MAR-1999 (first entry)

XX DE Mouse derived RT3 phage antibody light chain pattern C genetic sequence.

XX KW Catalytic; antibody; phage display; immunising; phage expression vector;
 KW prodrug; scfv.

XX OS Mus sp.

XX PN US5855885-A.

XX PD 05-JAN-1999.

XX PF 14-JUL-1994; 94US-0273146.

XX PR 22-JAN-1993; 93US-0007684.

XX PR 14-JUL-1994; 94US-0273146.

XX (CHIS/) CHISWELL D.

XX PA (DARS/) DARSLEY M J.

XX PA (FITZ/) FITZGERALD K.

XX PA (KENT/) KENTEN J H.

XX PA (MART/) MARTIN M T.

XX PA (MCCA/) MCCAFFERTY J.

XX PA (SMIT/) SMITH R.

XX PA (TITM/) TITMAS R C.

XX PA (WILL/) WILLIAMS R O.

XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;

DR WPI: 1999-105036/09.

DR N-PSDB; AAX00879.

XX Production of catalytic antibodies displayed on bacteriophages -

PT comprises generating a gene library of antibody-derived domains

PT inserting coding into a phage expression vector and isolating the

PT catalytic antibodies

XX Example 4; Fig 11; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies

CC displayed on a phage. The method comprises: (a) generating a gene library

CC of antibody-derived domains; (b) inserting coding for the domains into a

CC phage expression vector; and (c) isolating the catalytic antibodies. The

CC phage expression vector incorporates a histidine peptide in tandem with a

CC myc peptide. The catalytic antibodies can be isolated by preparing an
 CC antigen; optionally immunising an animal with the antigen; generating a
 CC library of VH and VL domains from the immunised animal; cloning the VH
 CC and VL domains into a phage expression vector to generate phage display
 CC antibodies; selecting phage display antibodies which bind specifically
 CC to the antigen; screening the selected phage display antibodies for
 CC catalytic activity to substrate; and isolating the catalytic antibodies,
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug. The
 CC present sequence represents a genetic sequence of light chain PCR
 CC pattern C from mouse derived RT3 phage antibodies.

XX Sequence 92 AA;

Query Match 100.0%; Score 31; DB 20; Length 92;

Best Local Similarity 100.0%; Pred. No. 9.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

Db 42 ATSSLS 48

RESULT 5

AAW95476

ID AAW95476 standard; Protein; 92 AA.

XX AC AAW95476;

XX DT 29-MAR-1999 (first entry)

XX DE Mouse derived RT3 phage antibody light chain pattern A genetic sequence.

XX KW Catalytic; antibody; phage display; immunising; phage expression vector;
 KW prodrug; scfv.

XX OS Mus sp.

XX PN US5855885-A.

XX PD 05-JAN-1999.

XX PF 14-JUL-1994; 94US-0273146.

XX PR 22-JAN-1993; 93US-0007684.

XX PR 14-JUL-1994; 94US-0273146.

XX (CHIS/) CHISWELL D.

XX PA (DARS/) DARSLEY M J.

XX PA (FITZ/) FITZGERALD K.

XX PA (KENT/) KENTEN J H.

XX PA (MART/) MARTIN M T.

XX PA (MCCA/) MCCAFFERTY J.

XX PA (SMIT/) SMITH R.

XX PA (TITM/) TITMAS R C.

XX PA (WILL/) WILLIAMS R O.

XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;

PI Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;

DR WPI: 1999-105036/09.

DR N-PSDB; AAX00875.

XX Production of catalytic antibodies displayed on bacteriophages -

PT comprises generating a gene library of antibody-derived domains

PT inserting coding into a phage expression vector and isolating the

PT catalytic antibodies

XX Example 4; Fig 9A-F; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies

CC displayed on a phage. The method comprises: (a) generating a gene library

CC of antibody-derived domains; (b) inserting coding for the domains into a
 CC phage expression vector; and (c) isolating the catalytic antibodies. The
 CC phage expression vector incorporates a histidine peptide in tandem with a
 CC myc peptide. The catalytic antibodies can be isolated by preparing an
 CC antigen; optionally immunising an animal with the antigen; generating a
 CC library of VH and VL domains from the immunised animal; cloning the VH
 CC and VL domains into a phage expression vector to generate phage display
 CC antibodies; selecting phage display antibodies which bind specifically
 CC to the antigen; screening the selected phage display antibodies for
 CC catalytic activity to substrate; and isolating the catalytic antibodies
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug. The
 CC present sequence represents a genetic sequence of light chain pattern A
 CC from mouse derived RT3 phage antibodies.

SQ Sequence 92 AA;
 Query Match 100.0%; Score 31; DB 20; Length 92;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATSSLS 7
 |||||
 Db 42 ATSSLS 48

RESULT 6
 AAW70954
 ID AAW70954 standard; protein; 95 AA.
 AC AAW70954;
 DT 14-OCT-1998 (first entry)
 DE Light chain of monoclonal antibody RS-255.
 KW Pathogenic virus; tropism: mucosa; CDR region; monoclonal antibody;
 KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
 KW viral infection; inhibit; fusion; protection; transcription;
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
 OS Mus sp.

XX FR2758331-A1.
 XX 17-JUL-1998.
 XX 14-JAN-1997; 97FR-0000300.
 XX 14-JAN-1997; 97FR-0000300.
 XX (UYBO-) UNIV BOURGOGNE.
 XX Bourgeois C, Kohli E, Pothier P;
 XX WPI: 1998-390320/34.
 XX New peptide(s) recognising viral epitope with tropism to mucosa -
 XX useful for, e.g. diagnosing, preventing and treating viral
 XX infection(s)
 XX Disclosure; Fig 2: 51pp; French.

XX The present sequence represents the light chain of monoclonal antibody
 CC RS-255, which is directed against the respiratory syncytial virus (RSV).
 CC The specification describes peptides which recognise, by
 CC antigen-antibody type reactions, at least 1 epitope of a pathogenic virus
 CC having tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous
 CC to CDR regions of monoclonal antibodies specific for RSV. AAW70917-28 are
 CC analogous to CDR regions of monoclonal antibodies specific for site III
 CC or IV of the VP6 protein of rota virus (RV). The peptides can neutralise
 CC viral infections and may also inhibit fusion between infected and

CC uninfected cells or cells and viruses. They provide passive or active
 CC protection and/or inhibit transcription of the virus, so are useful as
 CC antiviral agents or for prophylaxis, in human or veterinary medicine. The
 CC peptides can be labelled and used to diagnose infection or contamination
 CC by the virus. The peptides are particularly directed against RSV or RS
 CC but may also be used against papilloma, adeno, entero, polio, influenza
 CC or immune deficiency viruses.

SQ Sequence 95 AA;
 Query Match 100.0%; Score 31; DB 19; Length 95;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATSSLS 7
 |||||
 Db 37 ATSSLS 43

RESULT 7
 ABP33764
 ID ABP33764 standard; Protein; 97 AA.
 AC ABP33764;
 XX 08-JUL-2002 (first entry)
 DE Human transport protein-like ORF2737 protein, SEQ ID NO:5474.

XX Human: ORF; open reading frame; ORFX; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibitor; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
 KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiatic; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide.

OS Homo sapiens.

XX WO200190366-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17076.

XX 24-MAY-2000; 2000US-206690P.

XX (CURA-) CURAGEN CORP.

XX Leach MD, Shinkets RA;

XX WPI: 2002-106200/14.

XX N-PSDB; ABN77790.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation

XX Claim 10; Page 1619-1620; 2508pp; English.

XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX

CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening for modulators of ORFX expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases.

SQ Sequence 97 AA;

Query Match 100.0%; Score 31; DB 23; Length 97;
 Best Local Similarity 100.0%; Pred. No. 10;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLSLS 7

Db 52 ATSSLSLS 58

RESULT 8

AAW27121

ID AAW27121 standard; Protein; 107 AA.

XX AC AAW27121;

XX DT 04-JAN-1998 (first entry)

XX DE Murine antibody light chain variable region consensus.

XX KW Monoclonal antibody 11D10; anti-idiotype antibody; mucin;

XX KW human milk fat globule; HMF; tumour; breast cancer; vaccine.

XX OS Mus musculus.

XX FH Key

XX FT Location/Qualifiers

XX FT 24..34

XX FT /label= CDR1

XX FT /note= "complementarity determining region 1"

XX FT 50..56

XX FT /label= CDR2

XX FT /note= "complementarity determining region 2"

XX FT 88..96

XX FT /label= CDR3

XX FT /note= "complementarity determining region 3"

XX W09722699-A2.

PN 26-JUN-1997.

XX PD 19-DEC-1996; 96WO-US20757.

XX PF 13-DEC-1996; 96US-0575762.

XX PR

PR 20-DEC-1995; 95US-0575762.

PR 26-JAN-1996; 96US-0591965.

XX PA (KENT) UNIV KENTUCKY.

XX PI Chatterjee M, Chatterjee SK, Foon KA;

XX WPI; 1997-341690/31.

XX Monoclonal anti-idiotype antibody 11D10 - elicits immune response
 XX against human milk fat globule disease associated tumours,
 XX especially breast cancer

XX Example 2; Fig 26C; 130pp; English.

XX This polypeptide sequence comprises a consensus sequence of murine
 CC light chain variable regions (VL) selected on the basis of identity
 CC to the VL region (see W27119) of monoclonal anti-idiotype antibody
 CC 11D10. The sequences were obtained from a GenBank database
 CC search. A VH consensus (W27122) was also produced. 11D10 has at
 CC least 18 departures from the consensus sequences (7 in the light
 CC chain and 11 in the heavy chain). 8 Occur within CDRs and 10
 CC outside CDRs. 11D10 polypeptides and polynucleotides can be
 CC used in vaccines and pharmaceutical compositions for the treatment
 CC of human milk fat globule-associated diseases such as breast
 CC cancer.

SQ Sequence 107 AA;

Query Match 100.0%; Score 31; DB 18; Length 107;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLSLS 7

Db 50 ATSSLSLS 56

RESULT 9

AAAY90824

ID AAY90824 standard; Protein; 107 AA.

XX AC AAY90824;

XX DT 29-AUG-2000 (first entry)

XX DE 520C9 hybridoma VL domain SEQ ID NO:26.

XX KW Antigen binding site; immunoglobulin; cancer antigen; immunological;
 KW antibody; tumour; human; cancer; cytostatic; hybridoma;
 KW specific binding assay; affinity purification; drug targeting;
 KW toxin targeting; imaging; genetic; therapeutic.

XX OS Homo sapiens.

XX PN US6054561-A.

XX PD 25-APR-2000.

XX PF 07-JUN-1995; 95US-0483749.

XX PR 21-MAR-1986; 86US-0842476.

XX PR 08-MAY-1988; 88US-0190778.

XX PR 08-FEB-1984; 84US-0577976.

XX PR 11-JAN-1985; 85US-0690750.

XX PR 11-AUG-1994; 94US-0288981.

XX PA (CHIR) CHIRON CORP.

XX PI Ring DB;

XX WPI; 2000-338508/29.

XX N-PSDB; AAA38908.

XX Monoclonal antibody capable of binding to human breast cancer antigen
PT useful for affinity purification, drug or toxin targeting, imaging, and
PT treating cancer
XX
XX Disclosure; Fig 13; 57pp; English.
XX
XX The present invention describes a monoclonal antibody (MAB) (I) that
CC binds to a human breast cancer antigen that is also bound by MAB 454C11
CC and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
CC described is a hybridoma that produces (I). (I) is useful in specific
CC binding assays, affinity purification, drug or toxin targeting, imaging,
CC and genetic or immunological therapeutics for various cancers. The
CC present sequence represents a VL domain derived from a 520C9 hybridoma,
CC which is used in the exemplification of the present invention.
XX
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 31; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSLDS 7
|||||||
Db 50 ATSSLDS 56

RESULT 10
AAR21310
ID AAR21310 standard; Protein; 108 AA.
XX
AC AAR21310;
XX
XX 21-MAY-1992 (first entry)
XX Light chain of M1f clone.
DE
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 25..34
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 89..96
FT /label= CDR3
XX
XX WO9201047-A.
PN
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1991; 91WO-GB01134.
PF
XX 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PA
XX
XX McCafferty J, Pope AP, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GB, Bonnett TP;
XX WPI; 1992-056862/07.
XX
XX Producing members of specific binding pairs - by expression in
PT

PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
XX Example 46; Fig 52; 109pp; English.
XX

CC The sequence is the light chain of clone M1F encoding an scFv frag-
CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC The DNA encoding the chain was amplified from a cDNA library prepd.
CC from the spleen of an unimmunised mouse. The corresponding heavy
CC chain was also amplified from an existing construct, pSV1-VHD1.3
CC (Ward et al, 1989). The two fragments were assembled via a linker
CC to prepare an scFv construct which was ligated into the fdCAT2
CC vector for expression on the surface of fd bacteriophage. In this
CC way, the VL domain was replaced by a library of VL domains to allow
CC for selection of a broader range of antibody specificities. Several
CC clones were isolated which bound to TEL (the parent antibody D1.3
CC binds exclusively to HEL). The sequences of the light chains of
CC two of these clones, MFL and M21 are given in AAR21310 and AAR21311
CC respectively. The D1.3 light chain is given in AAR21309.
CC See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.
XX

SQ Sequence 108 AA;
Query Match 100.0%; Score 31; DB 13; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
|||||||
Db 50 ATSSLDS 56

RESULT 11
AAY44587
ID AAY44587 standard; Protein; 108 AA.
XX
AC AAY44587;
XX

DT 04-APR-2000 (first entry)
XX

DE Mouse anti-IL-18 antibody light chain variable region.
XX

KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
KW antiinflammatory; immunosuppressive; leucocytopenic; antialgic;
KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
KW immunopathy; inflammatory disorder; immunoreaction.
XX

OS Mus musculus.
XX

PN EP974600-A2.
XX

PD 26-JAN-2000.
XX

PF 24-JUN-1999; 99EP-0304977.
XX

PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX

PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX

DR WPI; 2000-118341/11.
XX

DR N-PSDB; AAZ49534.
XX

PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX

PS Claim 5; Page 17; 36pp; English.
XX

CC The present protein sequence is the mouse anti-Interleukin-18 antibody
 CC light chain variable region (VL) encoded by cDNA derived from hybridoma
 CC #125-2H. The nucleotide sequence is used in the production of recombinant
 CC monoclonal antibody #125-2HmAb, which is capable of neutralising
 CC biological activities of interleukin-18. The antibody has antialgic,
 CC antiinflammatory, immunosuppressive, leucocytopenic, antipyretic,
 CC antiallergic and hepatotropic activity and can be used for prevention and
 CC treatment of autoimmune diseases, immunopathies and inflammatory
 CC disorders caused by excessive immunoreaction.

XX Sequence 108 AA;

Query Match 100.0%; Score 31; DB 21; Length 108;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
 Db 50 ATSSLS 56

RESULT 12

AAW18271
 ID AAW18271 standard; peptide; 109 AA.

XX AC AAW18271;

XX DT 09-JAN-1998 (first entry)

XX DE PrP 37 light chain variable region.

XX Prion protein; Prp; heavy chain variable region; antibody; scrapie;
 XX light chain variable region; Prp-Sc; pathogen; fatal familial insomnia;
 KW central nervous system spongiform encephalopathy; human; therapy;
 KW transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
 KW bovine spongiform encephalopathy; feline spongiform encephalopathy;
 KW Serstmann-Strassler-Scheinker Disease.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Region 1..23 /note= "framework region 1"

FT Region 24..34 /note= "complementarity determining region 1"

FT Region 35..49 /note= "framework region 2"

FT Region 50..56 /note= "complementarity determining region 2"

FT Region 57..88 /note= "framework region 3"

FT Region 89..97 /note= "complementarity determining region 3"

FT Region 98..109 /note= "framework region 4"

XX WO9710505-A1.

XX 20-MAR-1997.

XX 13-SEP-1996; 96WO-US14840.

XX 14-SEP-1995; 95US-0528104.

XX (REGC) UNIV CALIFORNIA.

XX Burton DR, Prusiner SB, Williamson RA;

XX WPI; 1997-202357/18.

XX New antibodies to the scrapie isoform of prion protein - used for
 PT detection of infectious prion proteins or for treating disease such
 PT as BSE, CJD or scrapie

XX PS

Example 9; Fig 6; 99pp; English.

CC AAW18266-W18285 represent portions of the antibodies of the invention.
 CC The antibodies of the invention are able to bind the scrapie isoform of
 CC prion protein PrP-Sc in situ. Prions are infectious pathogens that cause
 CC central nervous system spongiform encephalopathies in humans and
 CC animals. The scrapie isoform of the prion protein (PrP-Sc) is necessary
 CC for both the transmission and pathogenesis of the transmissible
 CC neurodegenerative diseases of animals and humans. The antibodies can be
 CC used in a method of the invention for detecting human PrP-Sc in a source.
 CC The antibodies specifically bind to prion proteins associated with
 CC disease and do not bind to denatured PrP proteins not associated with
 CC disease. They can also bind to prion proteins of a specific species of
 CC mammals. They can also have the ability to neutralise infectious prions.
 CC The antibodies can be used for screening for the presence of prions in
 CC products such as pharmaceuticals, food or cosmetics. They can also be
 CC used for prion neutralisation to purify products, for extraction of prion
 CC proteins or for therapy, for diseases such as bovine spongiform
 CC encephalopathy, Creutzfeldt-Jakob Disease, fatal familial insomnia or
 CC Serstmann-Strassler-Scheinker Disease, scrapie or feline spongiform
 CC encephalopathies.

XX Sequence 109 AA;

Query Match 100.0%; Score 31; DB 18; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7

Db 50 ATSSLS 56

RESULT 13

AAW85910
 ID AAW85910 standard; peptide; 109 AA.

XX AC AAW85910;

XX DT 12-FEB-1999 (first entry)

XX DE PrP 37 light chain variable region.

XX PrP; PrP(Sc); scrapie; isoform; antibody; prion; CJD; screening;
 KW Creutzfeldt-Jakob disease; infectivity; assay; pharmaceutical; food;
 KW cosmetic; therapeutic; mouse.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Region 1..23 /note= "Framework 1"

FT Region 24..34 /note= "complementarity determining region 1 (CDR1)"

FT Region 35..49 /note= "Framework 2"

FT Region 50..56 /note= "complementarity determining region 2 (CDR2)"

FT Region 57..88 /note= "Framework 3"

FT Region 89..97 /note= "complementarity determining region 3 (CDR3)"

FT Region 98..109 /note= "Framework 4"

XX US5846533-A.

XX 08-DEC-1998.

XX 13-SEP-1996; 96US-0713939.

XX 13-SEP-1996; 96US-0713939.

PR 14-SEP-1995; 95US-0528104.
 XX (SCRI) SCRIPPS RES INST.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Burton DR, Prusiner SB, Williamson RA;
 XX
 DR WPI; 1999-058996/05.
 XX
 XX Antibody specific for scrapie isoform of prion protein - useful for
 PT diagnosis and therapy
 PT
 XX Example 9; Fig 6A-B; 58pp; English.
 PS
 XX The invention relates to an antibody that is capable of binding to
 CC native PrP(Sc), the scrapie isoform of prion protein (PrP). The antibody
 CC is produced by a method that comprises synthesising a library of
 CC antibodies on phages, contacting the phages with a composition containing
 CC PrP proteins, isolating phages that bind to native PrP(Sc) in situ,
 CC obtaining an antibody from the phages, and optionally analysing the
 CC phages to determine a nucleic acid sequence encoding an amino acid
 CC sequence to which the native PrP(Sc) binds. The antibody is used to
 CC detect disease-associated PrP, especially in Creutzfeldt-Jakob disease
 CC (CJD) and distinguish it from normal PrP. They can also be used to
 CC neutralise the infectivity of PrP(Sc). Assays using the antibodies can be
 CC used to screen for disease-associated PrP in pharmaceutical products,
 CC cosmetics and foods or for therapeutic purposes. Sequences AAW85908 to
 CC AAW85910 represent light chain variable regions of the phage clones
 CC generated by panning an IgG1 library from mouse D7282 against denatured
 CC PrP.
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 100.0%; Score 31; DB 20; Length 109;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSLDS 7
 DB ||||||
 50 ATSSLDS 56
 RESULT 14
 AAG65862
 ID AAG65862 standard; peptide; 109 AA.
 XX
 AC AAG65862;
 XX
 DT 11-FEB-2002 (first entry)
 DE Anti-PrP antibody light chain variable region fragment.
 XX
 XX PrP: prion protein; Creutzfeldt-Jakob disease; familial insomnia; PrP-Sc;
 KW scrapie; Gerstmann-Strassler-Scheinker disease; anti-PrP antibody.
 KW
 OS Mus sp.
 OS
 XX US6290954-B1.
 XX
 PN 18-SEP-2001.
 XX
 XX 06-MAR-1998; 98US-0036579.
 PF
 XX 13-SEP-1996; 96US-0713939.
 PR
 PR 14-SEP-1995; 95US-0528104.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Prusiner SB, Williamson RA, Burton DR;
 PI
 XX WPI; 2001-637939/73.
 DR
 XX Detecting a scrapie isoform of the prion protein (PrP-Sc) in a source,
 PT

PT particularly useful for detecting e.g. Creutzfeldt-Jakob disease or
 PT Gerstmann-Strassler-Scheinker disease, by contacting the source with
 PT PrP-Sc antibodies
 XX
 PS Example 9; Fig 6A-B; 58pp; English.
 XX
 XX The invention provides a method for detecting a scrapie isoform of the
 CC prion protein (PrP-Sc) in a source. The method involves contacting the
 CC source suspected of containing native PrP-Sc with a diagnostic amount of
 CC an antibody characterized by its ability to bind to native PrP-Sc in
 CC situ. The method is useful for detecting PrP-Sc in a source, which is
 CC particularly useful for detecting Creutzfeldt-Jakob disease, fatal
 CC familial insomnia or Gerstmann-Strassler-Scheinker disease. Sequences
 CC AAG65856-862 represent amino acid sequences of heavy and light chain
 CC variable regions of anti-PrP antibodies.
 XX
 XX Sequence 109 AA;
 SQ
 Query Match 100.0%; Score 31; DB 22; Length 109;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSLDS 7
 DB ||||||
 50 ATSSLDS 56
 RESULT 15
 ABP51796
 ID ABP51796 standard; Protein; 109 AA.
 XX
 AC ABP51796;
 XX
 DT 03-OCT-2002 (first entry)
 DE Anti-prion protein (PrP) antibody related protein SEQ ID NO:74.
 XX
 XX Prion protein; PrP; scrapie; PrPSc; prion disease; immunoassay;
 KW detection; anti-prion protein antibody; anti-PrP antibody.
 KW
 XX Mus sp.
 OS Synthetic.
 OS
 XX US6372214-B1.
 PN
 XX 16-APR-2002.
 PD
 XX 13-APR-2000; 2000US-0550374.
 PF
 XX 13-SEP-1996; 96US-0713939.
 PR
 PR 06-MAR-1998; 98US-0036579.
 PR
 PR 14-SEP-1995; 95US-0528104.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 PA (SCRI) SCRIPPS RES INST.
 XX
 XX Prusiner SB, Williamson RA, Burton DR;
 PI
 XX WPI; 2002-433675/46.
 DR
 XX Immunoassays for detecting scrapie isoforms of prion protein (PrPSc)
 PT and for purifying PrPSc from samples, useful e.g. in diagnosing PrPSc
 PT disease and testing pharmaceuticals for contamination
 XX
 PS Example 9; Fig 6; 58pp; English.
 XX
 XX The present invention describes methods for detecting scrapie isoforms
 CC of prion protein (PrPSc) infection in dead animals, purifying materials
 CC suspected of containing PrPSc proteins and treating materials, using
 CC antibodies specific for PrPSc. Also described: (1) method of determining
 CC PrPSc infection in a dead animal, comprising: (a) extracting tissue from
 CC an animal that has died; (b) contacting the tissue with an antibody
 CC characterised by its ability to bind to native PrPSc in situ (the

CC antibody binds to a form of PrPsc specific to the animal that has died);
CC and (c) determining if the antibody has bound to PrPsc (the presence of
CC PrPsc in the tissue is indicative of PrPsc infection); (2) a method of
CC purifying a material suspected of containing a PrPsc protein, comprising:
CC (a) contacting the material with an antibody (characterized by its
CC ability to bind native PrPsc in situ) which is bound to a support
CC surface; and (b) removing material not bound to the antibody; (3) a
CC method of treating a material, comprising applying (to the material) an
CC antibody that binds native PrPsc in situ. The methods are used for
CC diagnosing and detecting prion disease (scrapie) in dead animal tissue
CC (i.e. immunoassays), for separating PrPsc proteins from biological
CC samples (i.e. immunoprecipitation) and for treating materials. The present
CC sequence represents an anti-prion protein (PrP) antibody related protein
CC sequence, which is used in an example from the present invention.
XX

SQ Sequence 109 AA;

Query Match 100.0%; Score 31; DB 23; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
Db 50 ATSSLDS 56
|||||||

Search completed: March 10, 2003, 16:56:56
Job time : 20.7931 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 25.4483 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
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22: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	47	100.0	9	21	Mouse anti-IL-18 a
2	47	100.0	90	16	Mouse derived high
3	47	100.0	90	16	Mouse derived high
4	47	100.0	92	20	Mouse derived RT3
5	47	100.0	92	20	Mouse derived RT3
6	47	100.0	107	18	Murine antibody li
7	47	100.0	108	21	Mouse anti-IL-18 a
8	47	100.0	135	21	Mouse light chain
9	47	100.0	145	18	Murine monoclonal
10	47	100.0	145	20	Antibody 11D10 lig

11	47	100.0	237	21	AA44595	EscFv#125-2H recom
12	47	100.0	243	21	AA44596	EscFv#125-2H. HT re
13	47	100.0	252	23	AAU72863	P4-14 single chain
14	47	100.0	257	23	AAU72869	p5-11 single chain
15	47	100.0	499	23	AAU72872	3B10P4-14 bispeci
16	43	91.5	9	19	AAW70946	CDR3 of the light
17	43	91.5	95	19	AAW70954	Light chain of mon
18	42	89.4	108	13	AAW21310	Light chain of M1f
19	42	89.4	109	18	AAW18271	PrP 37 light chain
20	42	89.4	109	20	AAW85910	PrP 37 light chain
21	42	89.4	109	22	AAW65862	Anti-PrP antibody
22	42	89.4	109	23	ABP51796	Anti-prion protein
23	42	89.4	146	4	AAW30251	Sequence of the le
24	40	85.1	95	18	AAW18269	PrP 81 light chain
25	40	85.1	95	20	AAW85908	PrP 81 light chain
26	40	85.1	95	22	AAW65860	Anti-PrP antibody
27	40	85.1	95	23	ABP51794	Anti-prion protein
28	40	85.1	109	18	AAW18270	PrP 28 light chain
29	40	85.1	109	20	AAW85909	PrP 28 light chain
30	40	85.1	109	22	AAW65861	Anti-PrP antibody
31	40	85.1	109	23	ABP51795	Anti-prion protein
32	40	85.1	312	22	ABW09185	Acinetobacter calc
33	40	85.1	321	22	ABW09186	Acinetobacter calc
34	39	83.0	107	22	ABW62771	Human HIV-1 monocl
35	39	83.0	129	14	AAW38672	VX325-JK2. Homo s
36	37	78.7	107	15	AAW54308	Anti-HIV gp120 imm
37	37	78.7	107	17	AAW01266	VL region of HIV n
38	37	78.7	107	21	AAW95118	Anti-gp120 antibod
39	37	78.7	107	21	AAW98227	Anti-gp120 antibod
40	37	78.7	113	21	AAW18855	Amino acid sequenc
41	37	78.7	113	21	AAW18867	Amino acid sequenc
42	37	78.7	113	21	AAW18875	Amino acid sequenc
43	37	78.7	113	21	AAW18877	Amino acid sequenc
44	36	76.6	9	18	AAW24551	CDR #3 of r101-2 1
45	36	76.6	108	15	AAW54316	Anti-HIV gp120 imm

ALIGNMENTS

RESULT 1
AA44591
ID AA44591 standard; Protein; 9 AA.
AC AA44591;
DT 04-APR-2000 (first entry)
XX
DE Mouse anti-IL-18 antibody VL complementarity-determining region-3.
XX
KW Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
KW complementarity-determining region; CDR; hybridoma #125-2H; mouse;
KW monoclonal antibody #125-2HmAb; Interleukin-18; antiinflammatory;
KW immunosuppressive; leucocytopenic; antialgic; antipyretic;
KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
KW inflammatory disorder; immunoreaction.
XX
OS Mus musculus.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
XX
PR 12-OCT-1998; 98JP-0289044.
XX
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX

PT catalytic antibodies
 XX Example 4; Fig 9A-F; 117pp; English.
 XX The invention relates to methods for producing catalytic antibodies
 CC displayed on a phage...The method comprises: (a) generating a gene library
 CC of antibody-derived domains; (b) inserting coding for the domains into a
 CC phage expression vector; and (c) isolating the catalytic antibodies. The
 CC phage expression vector incorporates a histidine peptide in tandem with a
 CC myc peptide. The catalytic antibodies can be isolated by preparing an
 CC antigen; optionally immunising an animal with the antigen; generating a
 CC library of VH and VL domains from the immunised animal; cloning the VH
 CC and VL domains into a phage expression vector to generate phage display
 CC antibodies; selecting phage display antibodies which bind specifically
 CC to the antigen; screening the selected phage display antibodies for
 CC catalytic activity to substrate; and isolating the catalytic antibodies,
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug. The
 CC present sequence represents a genetic sequence of light chain pattern A
 CC from mouse derived Rt3 phage antibodies.
 XX SQ Sequence 92 AA;
 Query Match 100.0%; Score 47; DB 20; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOYASSPYT 9
 |||||
 Db 81 LOYASSPYT 89
 RESULT 6
 AAW27121
 ID AAW27121 standard; Protein; 107 AA.
 AC AAW27121;
 XX 04-JAN-1998 (first entry)
 XX Murine antibody light chain variable region consensus.
 DE Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
 KW human milk fat globule; HMF; tumour; breast cancer; vaccine.
 XX Mus musculus.
 OS
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50..56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 88..96
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 XX WO9722699-A2.
 PN 26-JUN-1997.
 XX 19-DEC-1996; 96WO-US20757.
 XX 13-DEC-1996; 96US-0575762.
 PR 20-DEC-1995; 95US-0575762.
 PR 26-JAN-1996; 96US-0591965.
 XX (KENT) UNIV KENTUCKY.
 PA Chatterjee M, Chatterjee SK, Foon KA;
 PI
 XX

DR WPI; 1997-341690/31.
 XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer
 XX Example 2; Fig 26C; 130pp; English.
 PS This polypeptide sequence comprises a consensus sequence of murine
 XX light chain variable regions (VL) selected on the basis of identity
 CC to the VL region (see W27119) of monoclonal anti-idiotypic antibody
 CC 11D10. The sequences were obtained from a GenBank database
 CC search. A VH consensus (W27122) was also produced. 11D10 has at
 CC least 18 departures from the consensus sequences (7 in the light
 CC chain and 11 in the heavy chain). 8 Occur within CDRs and 10
 CC outside CDRs. 11D10 polypeptides and polynucleotides can be
 CC used in vaccines and pharmaceutical compositions for the treatment
 CC of human milk fat globule-associated diseases such as breast
 CC cancer.
 XX SQ Sequence 107 AA;
 Query Match 100.0%; Score 47; DB 18; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOYASSPYT 9
 |||||
 Db 89 LOYASSPYT 97
 RESULT 7
 AAY44587
 ID AAY44587 standard; Protein; 108 AA.
 XX AAY44587;
 AC AAY44587;
 XX 04-APR-2000 (first entry)
 XX Mouse anti-IL-18 antibody light chain variable region.
 DE Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL;
 KW hydridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; Interleukin-18;
 KW antiinflammatory; immunosuppressive; leucocytopoietic; antialgic;
 KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
 KW immunopathy; inflammatory disorder; immunoreaction.
 XX Mus musculus.
 OS
 XX EP974600-A2.
 PN 26-JAN-2000.
 XX 24-JUN-1999; 99EP-0304977.
 PF 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX WPI; 2000-118341/11.
 DR N-PSDB; AA249534.
 XX New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX Claim 5; Page 17; 36pp; English.
 PS The present protein sequence is the mouse anti-Interleukin-18 antibody
 CC

CC light chain variable region (VL) encoded by cDNA derived from hybridoma
 CC #125-2H. The nucleotide sequence is used in the production of recombinant
 CC monoclonal antibodies #125-2HAb, which is capable of neutralising
 CC biological activities of interleukin-18. The antibody has antiallgic,
 CC antiinflammatory, immunosuppressive, leucocytopenic, antipyretic,
 CC antiallergic and hepatotropic activity and can be used for prevention and
 CC treatment of autoimmune diseases, immunopathies and inflammatory
 CC disorders caused by excessive immunoreaction.
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 47; DB 21; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LOYASSPYT 9
 Db 89 LOYASSPYT 97
 |||||

RESULT 8
 AAY44599
 ID AAY44599 standard; Protein; 135 AA.
 XX
 AC AAY44599;
 XX
 DT 04-APR-2000 (first entry)
 DE Mouse light chain variable region encoded by PCR A product.
 XX
 KW Mouse light chain variable region; VL: variable region light chain;
 KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
 KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
 KW hematopoietic; leukocytopenic; antiallgic; antipyretic.
 XX
 OS Mus musculus.
 OS Synthetic.

XX
 PN EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 PF 24-JUN-1999; 99EP-0304977.
 XX
 PR 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX
 DR WPI: 2000-118341/11.
 DR N-PSDB; AAZ49548.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases .
 XX
 PS Disclosure; Page 28-29; 32pp; English.

XX
 CC The present sequence is the mouse light chain variable region. This was
 CC encoded by a recombinant DNA is derived from PCR A which amplifies
 CC antibody light chain variable region (VL). The transformant produced
 CC using the VL gene was used transform competent E. coli cells. The peptide
 CC produced by transformants neutralises interleukin-18. This is useful for
 CC treating and preventing immunopathies, inflammatory disorders and
 CC autoimmune diseases which are caused by excessive immunoreaction. The
 CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
 CC hematopoietic, leucocytopenic, antiallgic, antipyretic and hepatic
 CC -function improving activities.
 XX
 SQ Sequence 135 AA;

Query Match 100.0%; Score 47; DB 21; Length 135;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LOYASSPYT 9
 Db 109 LOYASSPYT 117
 |||||

RESULT 9
 AAW27119
 ID AAW27119 standard; Protein; 145 AA.
 XX
 AC AAW27119;
 XX
 DT 04-JAN-1998 (first entry)
 DE Murine monoclonal anti-idiotypic antibody 11D10 VL region.
 XX
 KW Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
 KW human milk fat globule; HMFG; tumour; breast cancer; vaccine.
 XX
 OS Mus musculus.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT /label= 21..145
 FT Region /label= Mat_protein
 FT /label= 21..43
 FT /label= FRI
 FT /note= "framework region 1"
 FT /label= 44..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 55..69
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 70..76
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 77..108
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 109..117
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Region 118..127
 FT /label= FRI
 FT /note= "framework region 4"

XX
 PN WO9722699-A2.
 XX
 PD 26-JUN-1997.
 XX
 PF 19-DEC-1996; 96WO-US20757.
 XX
 PR 13-DEC-1996; 96US-0575762.
 PR 20-DEC-1995; 95US-0575762.
 PR 26-JAN-1996; 96US-0591965.
 XX
 PA (KENT) UNIV KENTUCKY.
 XX
 PI Chatterjee M, Chatterjee SK, Foon KA;
 XX
 DR WPI; 1997-341690/31.
 DR N-PSDB; AAT85149.
 XX
 KW Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer
 XX

PS Claim 9; Page 94; 130pp; English.

XX This polypeptide sequence comprises the light chain variable region

CC (VL) of monoclonal anti-idiotypic antibody 11D10 produced by

CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising

CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic

CC response. It elicits an immune response against a specific epitope

CC of a high mol.wt. mucin of human milk fat globule (HMFG). It

CC induces an immunological response to HMFG in mice, rabbits, monkeys

CC and patients with advanced HMFG-associated tumours. Pharmaceutical

CC compositions and vaccines comprising 11D10, 11D10 polypeptides

CC and/or 11D10 polynucleotides (See also AAR85149-50) are claimed.

CC Also claimed are diagnostic kits and methods of using 11D10, 11D10

CC polypeptides and/or 11D10 polynucleotides, including methods of

CC treating HMFG-associated tumours. 11D10 is also used in a claimed

CC method of palliating HMFG-associated disease and in claimed kits to

CC detect or quantify anti-HMFG antibody.

XX

SQ Sequence 145 AA;

Query Match 100.0%; Score 47; DB 18; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9

DB 109 LOYASSPYT 117

RESULT 10

AAW87593

ID AAW87593 standard; Protein; 145 AA.

XX

AC AAW87593;

XX

DT 16-MAR-1999 (first entry)

XX

DE Antibody 11D10 light chain variable region.

XX

KW Murine; mouse; antibody; light chain; variable region; anti-idiotypic;

KW human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Peptide 1..20 /note= "signal peptide"

FT Protein 21..999 /note= "mature protein"

FT Region 21..43 /label= framework_1

FT Domain 44..54 /label= CDR1

FT /label= CDR1

FT /note= "complementarity determining region 1"

FT Region 55..69 /label= framework_2

FT Misc-difference 55 /note= "encoded by TGG"

FT Domain 70..76 /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 77..108 /label= framework_3

FT Domain 109..117 /label= CDR3

FT /note= "complementarity determining region 3"

FT Region 118..127 /label= framework_4

XX

PN W09856419-A1.

XX

PD 17-DEC-1998.

XX

PF 12-JUN-1998; 98WO-US12250.

XX

PR 11-JUN-1998; 98US-0096244.

PR 13-JUN-1997; 97US-0049540.

XX

PA (KENT) UNIV KENTUCKY RES FOUND.

XX

PI Chatterjee M, Foon KA;

XX

DR WPI: 1999-060029/05.

DR N-PSDB; AAV83772.

XX

PT Delaying development of, or treating, HMFG-associated tumours -

PT using anti-idiotypic antibody 11D10 raised against antibodies to

PT human milk fat globule protein

XX

PS Disclosure; Fig 1; 54pp; English.

XX

CC This sequence represents the light chain variable region of the murine

CC antibody 11D10. This anti-idiotypic antibody is used to delay the

CC development of, or treat, a human milk fat globule (HMFG) associated

CC tumour in an individual having low tumour burden. The antibody 11D10

CC is used to prevent the recurrence of HMFG-associated tumours e.g. for

CC ovarian, non-small cell lung and pancreatic carcinoma, especially for

CC treating breast tumours.

XX

SQ Sequence 145 AA;

Query Match 100.0%; Score 47; DB 20; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9

DB 109 LOYASSPYT 117

RESULT 11

AAW44595

ID AAY44595 standard; Protein; 237 AA.

XX

AC AAY44595;

XX

DT 04-APR-2000 (first entry)

XX

DE EscFv#125-2H recombinant protein.

XX

KW EscFv#125-2H recombinant protein; interleukin-18; mouse;

KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;

KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopenic;

KW antialgic; antipyretic.

XX

OS Mus musculus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Domain 1..113 /note= "Heavy chain variable region"

FT Domain 114..130 /note= "Glycine-serine linker"

FT Domain 131..237 /note= "Light chain variable region"

XX

PN EP974600-A2.

XX

PD 26-JAN-2000.

XX

PF 24-JUN-1999; 99EP-0304977.

XX

PR 24-JUN-1998; 98JP-0177580.

PR 12-OCT-1998; 98JP-0289044.

PR 22-DEC-1998; 98JP-0365023.

XX

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PA XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
PI XX WPI; 2000-118341/11.
XX N-PSDB; AA249542.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
XX Claim 8; Page 19-20; 32pp; English.
XX
CC The present sequence is EscFv#125-2H protein encoded by recombinant cDNA
CC pEscFv#125-2H for neutralising interleukin-18. The protein is produced
CC from hybridoma #125-2H by transforming pEscFv#125-2H in competent
CC E. coli cells. This is useful for treating and preventing immunopathies,
CC inflammatory disorders and autoimmune diseases which are caused by
CC excessive immunoreaction. The protein has anti-allergic,
CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopenetic,
CC antialgic, antipyretic and hepatic-function improving activities.
XX
SQ Sequence 237 AA;

Query Match 100.0%; Score 47; DB 21; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
IIIIIIIII

Dd 219 LOYASSPYT 227

RESULT 12

AAY44596

ID AAY44596 standard; Protein; 243 AA.

XX AC AAY44596;

XX 04-APR-2000 (first entry)

DE EscFv#125-2H.HT recombinant protein.

XX EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopenetic;
KW antialgic; antipyretic.

XX OS Mus musculus.
OS Synthetic.

XX Key Location/Qualifiers
FH Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"

XX EP974600-A2.
XX 26-JAN-2000.
XX 24-JUN-1999; 99EP-0304977.
XX 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
PI XX

XX Example 7; Fig 16; 114pp; English.
 XX The invention relates to a multifunctional polypeptide comprising a
 CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.
 XX Sequence 252 AA;
 SQ

Query Match 100.0%; Score 47; DB 23; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
 Db 222 LQYASSPYT 230
 |||||

RESULT 14
 AAU72869
 ID AAU72869 standard; Protein; 257 AA.
 XX
 AC AAU72869;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE P5-11 single chain Fv.
 XX
 KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
 KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 XX
 OS Homo sapiens.
 XX
 PN WO200171005-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-MAR-2001; 2001WO-EP03414.
 XX
 PR 24-MAR-2000; 2000EP-0106467.
 XX
 PA (KUFE/) KUFER P.
 XX
 PI Kufer P, Riethmüller G, Lutterbuese R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 XX
 DR WPI; 2002-055119/07.
 DR N-PSDB; AAS97143.
 XX
 PT Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and
 PT domains which function as receptors or ligands, useful for treating

PT cancers and infectious diseases -
 XX Example 7; Fig 16; 114pp; English.
 XX The invention relates to a multifunctional polypeptide comprising a
 CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.
 XX Sequence 257 AA;
 SQ

Query Match 100.0%; Score 47; DB 23; Length 257;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
 Db 227 LQYASSPYT 235
 |||||

RESULT 15
 AAU72872
 ID AAU72872 standard; Protein; 499 AA.
 XX
 AC AAU72872;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE 3B10xP4-14 bispecific single chain Fv.
 XX
 KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
 KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 XX
 OS Homo sapiens.
 XX
 PN WO200171005-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-MAR-2001; 2001WO-EP03414.
 XX
 PR 24-MAR-2000; 2000EP-0106467.
 XX
 PA (KUFE/) KUFER P.
 XX
 PI Kufer P, Riethmüller G, Lutterbuese R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 XX
 DR WPI; 2002-055119/07.
 DR N-PSDB; AAS97146.
 XX
 PT Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and

PT domains which function as receptors or ligands, useful for treating
 PT cancers and infectious diseases -
 XX
 PS
 XX Example 5; Fig 16; 114pp; English.
 XX
 CC The invention relates to a multifunctional polypeptide comprising a
 CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated
 CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.

SQ Sequence 499 AA;
 Query Match 100.0%; Score 47; DB 23; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LOYASSPYT 9
 DB 469 LOYASSPYT 477
 |||||

Search completed: March 10, 2003, 16:56:56
 Job time : 25.483 secs

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OM protein - protein search, using sw model

Run On: March 10, 2003, 16:46:26 ; Search time 24.2759 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	70.4	127	11 Q925S9	Q925S9 mus musculus
2	37	68.5	479	15 Q84808	Q84808 puma lentiv
3	36	66.7	293	12 Q80851	Q80851 hydrangea m
4	36	66.7	305	16 Q82DQ5	Q82DQ5 yersinia pe
5	36	66.7	442	16 Q84377	Q84377 chlamydia t
6	36	66.7	548	10 Q9C618	Q9C618 arabidopsis
7	35	64.8	194	3 Q93950	Q93950 candida alb
8	35	64.8	211	2 Q9F8M9	Q9F8M9 carboxydoth
9	35	64.8	219	11 Q9QZ61	Q9QZ61 mus musculus
10	35	64.8	231	11 Q9WU10	Q9WU10 mus musculus
11	35	64.8	232	4 Q9H2W2	Q9H2W2 homo sapien
12	34	63.0	45	2 Q9ZG20	Q9ZG20 chlamydia t
13	34	63.0	160	17 Q8U198	Q8U198 pyrococcus
14	34	63.0	193	16 Q9JWK5	Q9JWK5 neisseria m
15	34	63.0	216	13 Q9PU79	Q9PU79 crocodylus
16	34	63.0	269	16 Q51586	Q51586 borrelia bu

17	34	63.0	285	10 Q41176	Q41176 luffa cylin
18	34	63.0	324	16 Q828X4	Q828X4 salmoneilla
19	34	63.0	330	10 Q94JV0	Q94JV0 arabidopsis
20	34	63.0	377	10 Q49495	Q49495 arabidopsis
21	34	63.0	471	16 Q9PK22	Q9PK22 chlamydia m
22	34	63.0	494	2 Q9AFS3	Q9AFS3 shigella fl
23	34	63.0	494	2 Q9VSH5	Q9VSH5 shigella fl
24	34	63.0	525	4 Q96N21	Q96N21 homo sapien
25	34	63.0	536	3 Q9UVS8	Q9UVS8 aspergillus
26	34	63.0	565	16 Q8XJE4	Q8XJE4 clostridium
27	34	63.0	610	2 Q93G04	Q93G04 lactobacill
28	34	63.0	644	16 Q98CV7	Q98CV7 rhizobium l
29	34	63.0	799	2 Q8RK21	Q8RK21 providencia
30	34	63.0	886	16 Q9CBY7	Q9CBY7 mycobacteri
31	33.5	62.0	370	5 Q8SUY4	Q8SUY4 encephalito
32	33	61.1	184	11 Q9DAP5	Q9DAP5 mus musculu
33	33	61.1	216	13 Q9PU23	Q9PU23 trachemys s
34	33	61.1	225	2 Q86118	Q86118 rhodobacter
35	33	61.1	237	3 Q08914	Q08914 saccharomyc
36	33	61.1	237	3 Q08992	Q08992 saccharomyc
37	33	61.1	245	12 Q9QKC4	Q9QKC4 rift valley
38	33	61.1	246	12 Q9QKC5	Q9QKC5 rift valley
39	33	61.1	312	10 Q8W0H8	Q8W0H8 triticum ae
40	33	61.1	312	11 Q8XM31	Q8XM31 clostridium
41	33	61.1	314	11 Q8VGN1	Q8VGN1 mus musculu
42	33	61.1	334	10 Q9LWU3	Q9LWU3 arabidopsis
43	33	61.1	346	16 Q86705	Q86705 streptomyce
44	33	61.1	349	16 Q9RUY4	Q9RUY4 deinococcus
45	33	61.1	366	15 Q92WQ5	Q92WQ5 rhizobium m

ALIGNMENTS

RESULT 1

Q925S9 ID Q925S9 PRELIMINARY; PRT; 127 AA.

AC Q925S9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Immunoglobulin light chain (Fragment).

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=99306687; PubMed=10380019;
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA Foon K.A., Chatterjee S.K.;
RT "Construction and characterization of a chimeric fusion protein
RT consisting of an anti-idiotypic antibody mimicking a breast cancer-
RT associated antigen and the cytokine GM-CSF.";
RL Hybridoma 18:193-202(1999).
DR EMBL; AFI124721; AAK55120.1;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1;
FT NON_TER 127; 127
SQ SEQUENCE 127 AA; 13794 MW; 13F61BEBB981FA5 CRC64;

Query Match 70.4%; Score 38; DB 11; Length 127;
Best Local Similarity 72.7%; Pred. No. 5.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
Db 44 RASQDIGINLH 54

RESULT 2

Q84808

```

ID Q84808 PRELIMINARY; PRT; 479 AA.
AC Q84808;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE GAG polyprotein [Contains: core protein(s) p24].
GN GAG.
OS Puma lentivirus 14.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=32615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94303200; PubMed=8030248;
RA Langley R.J., Hirsch V.M., O'Brien S.J., Adger-Johnson D.,
RA Goeken R.M., Olmsted R.A.
RT "Nucleotide sequence and analysis of puma lentivirus (PLV-14): genomic
RT organization and relationship to other lentiviruses.";
RL Virology 202; 853-864(1994).
CC 1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
DR EMBL; U03982; AAA67167.1; -.
DR HSP; P03351; IE1A.
DR InterPro; IPR000721; Gag_p24.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00607; Gag_p24; 1.
DR Pfam; PF00098; zfp_CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 2.
DR Core protein; Polyprotein.
KW SEQUENCE 479 AA; 52647 MW; 21C4190013B21242 CRC64;

Query Match 68.5%; Score 37; DB 15; Length 479;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
||| ||| ||| |||
Db 343 RACQDIGSTQY 353

RESULT 3
Q80851 PRELIMINARY; PRT; 293 AA.
ID Q80851;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 3a protein.
OS hydrangea mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=42812;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96290233; PubMed=8725121;
RA Ge X., Scott S.W.;
RT "The nucleotide sequence of hydrangea mosaic virus RNA 3 exhibits
RT similarity with the RNA 3 of tobacco streak virus.";
RL Virus Res. 40:57-63(1996).
DR EMBL; U35145; AAA80344.1; -.
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP; 1.
DR SEQUENCE 293 AA; 32112 MW; 734612E4A1934A75 CRC64;

Query Match 66.7%; Score 36; DB 12; Length 293;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
||| ||| ||| |||
Db 213 RASTDIASKRY 223

RESULT 4
Q80851 PRELIMINARY; PRT; 305 AA.
ID Q80851;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sugar binding protein.
GN RBSB OR YPO2501.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CO-92 / BIOVAR ORIENTALIS;
MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414152; CAC91306.1; -.
DR InterPro; IPR001761; Periplabp/LacI.
DR Pfam; PF00532; Peripla_BP_like; 1.
DR Complete proteome.
KW SEQUENCE 305 AA; 32433 MW; 148AD7DDE3FF559B CRC64;

Query Match 66.7%; Score 36; DB 16; Length 305;
Best Local Similarity 54.5%; Pred. No. 38;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
||| ||| ||| |||
Db 52 QAANDIGAKVY 62

RESULT 5
Q84377 PRELIMINARY; PRT; 442 AA.
ID Q84377;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein CT372.
GN CT372.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D/UW-3/CX;
MEDLINE=95000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
DR EMBL; AE001310; AAC67968.1; -.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 442 AA; 49399 MW; 12DF52703A827408 CRC64;

Query Match 66.7%; Score 36; DB 16; Length 442;
Best Local Similarity 80.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQDIGSKLY 11
||| ||| ||| |||
Db 327 ASQHISSKLY 336

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RESULT 6
Q9C6L8
ID Q9C6L8 PRELIMINARY; PRT; 548 AA.
AC Q9C6L8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 61.7 kDa protein.
GN F217.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eumids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltcher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL; AC079281; AAG50799.1; -.
KW Hypothetical protein.
SQ SEQUENCE 548 AA; 61719 MW; ACB3B0F801D27518 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 548;
Best Local Similarity 63.6%; Pred. No. 74;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
Db 48 KALYDIGAKLY 58

RESULT 7
Q93950
ID Q93950 PRELIMINARY; PRT; 194 AA.
AC Q93950;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE CTA6p (Fragment).
GN CTA6.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaiser B., Kunkel W., Saluz H.P., Munder T.;
RT "Identification of Candida albicans protein domains with
RT transcriptional activating properties in Saccharomyces cerevisiae.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006641; CAA07169.1; -.
FT NON_TER 1

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SQ SEQUENCE 194 AA; 22307 MW; F119E1A0A250F7B1 CRC64;

Query Match 64.8%; Score 35; DB 3; Length 194;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SQDIGSKLY 11
Db 46 SQQFGSKLY 54

RESULT 8
Q9F8M9
ID Q9F8M9 PRELIMINARY; PRT; 211 AA.
AC Q9F8M9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 4-hydroxybutyrate CoA transferase (Fragment).
OS Carboxydotherrmus hydrogenoformans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Peptococcaceae; Carboxydotherrmus.
OX NCBI_TaxID=129958;
RN [1]
RP SEQUENCE FROM N.A.
RA Gonzalez J.M., Robb F.T.;
RT "A genomic survey of the extreme thermophilic, CO-utilizing bacterium
RT Carboxydotherrmus hydrogenoformans.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244604; AAG23553.1; -.
DR InterPro; IPR003702; AcetylCoA_hydro.
DR Pfam; PF02550; AcetylCoA_hydro; 1.
KW Transferase.
FT NON_TER 1
FT NON_TER 211
SQ SEQUENCE 211 AA; 23149 MW; C3038601E0C79E82 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 211;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDIGSKLY 11
Db 183 ASQSIGTKIY 192

RESULT 9
Q9Q261
ID Q9Q261 PRELIMINARY; PRT; 219 AA.
AC Q9Q261;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mix-related homeobox protein (Fragment).
GN MIXL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu Y., Chen S.W., Gudas L.J.;
RT "mMix, a Mouse Mix-related Homeobox Gene Expressed in the Primitive
RT Streak.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF201959; AAF08314.1; -.
DR HSSP; P06601; 1EJL.
DR MGD; MGI:1351322; Mixl1.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.

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DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 219 AA; 23639 MW; BD729DF8F1C8D1C3 CRC64;

Query Match 64.8%; Score 35; DB 11; Length 219;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
Db 198 SEDIGSKL 205

RESULT 10
Q9H2W2 ID Q9H2W2 PRELIMINARY; PRT; 231 AA.
AC Q9H2W2
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mix-like homeobox protein (Homeobox protein MIX).
GN MIXL1 OR MIX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425184; PubMed=10495285;
RA Pearce J.J., Evans M.J.;
RL "Mxl, a mouse mix-like gene expressed in the primitive streak.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=EMBRYO;
RA Robb L., Hartley L., Begley C.G., Elefanti A.G.;
RT "Expression of the homeobox gene mXl is restricted to the primitive
RT streak of the gastrulating mouse embryo.";
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF135063; AAD25543.1; -.
DR EMBL; AF135473; AAK59867.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04800; -.
DR MGD; MGI:1351322; Mixl1.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 231 AA; 24844 MW; 59DA80A5E7E6EE33 CRC64;

Query Match 64.8%; Score 35; DB 11; Length 231;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
Db 210 SEDIGSKL 217

RESULT 11
Q9H2W2 ID Q9H2W2 PRELIMINARY; PRT; 232 AA.
AC Q9H2W2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mix-like homeobox protein 1 (Homeodomain protein MIX).
GN MIXL1 OR MIX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425184; PubMed=10495285;
RA Pearce J.J., Evans M.J.;
RL "Mxl, a mouse mix-like gene expressed in the primitive streak.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=EMBRYO;
RA Robb L., Hartley L., Begley C.G., Elefanti A.G.;
RT "Expression of the homeobox gene mXl is restricted to the primitive
RT streak of the gastrulating mouse embryo.";
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF135063; AAD25543.1; -.
DR EMBL; AF135473; AAK59867.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04800; -.
DR MGD; MGI:1351322; Mixl1.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 231 AA; 24844 MW; 59DA80A5E7E6EE33 CRC64;

Query Match 64.8%; Score 35; DB 11; Length 231;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
Db 210 SEDIGSKL 217

RESULT 11
Q9H2W2 ID Q9H2W2 PRELIMINARY; PRT; 232 AA.
AC Q9H2W2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mix-like homeobox protein 1 (Homeodomain protein MIX).
GN MIXL1 OR MIX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425184; PubMed=10495285;
RA Robb L., Hartley L., Begley C.G., Brodnicki T.C.,
RA Copeland N.G., Gilbert D.J., Jenkins N.A., Elefanti A.G.;
RT "Mix, a murine homolog of the Xenopus Mix.1 gene, is expressed in the
RT presumptive posterior region of the prestreak embryo and in the
RT primitive streak.";
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF211891; AAG35776.1; -.
DR EMBL; AF218357; AAK01479.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04801; -.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 232 AA; 24659 MW; 2E8A6A811799A8F0 CRC64;

Query Match 64.8%; Score 35; DB 4; Length 232;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
Db 211 SEDIGSKL 218

RESULT 12
Q9ZG20 ID Q9ZG20 PRELIMINARY; PRT; 45 AA.
AC Q9ZG20
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Procarboxypeptidase A complex component III (fragment).
OC Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
RT sequencing.";
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF087356; AAD04128.1; -.
DR EMBL; AF087356; AAD04128.1; -.
KW Carboxypeptidase.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5067 MW; FC99367724DF12F8 CRC64;

Query Match 63.0%; Score 34; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
Db 9 ASQVSSKLY 18
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RESULT 13
Q8U198
ID Q8U198 PRELIMINARY; PRT; 160 AA.
AC Q8U198;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Hypothetical protein PFI324.
GN PFI324.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VCL / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010237; AAL81448.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 160 AA; 18742 MW; 7E3B496DC037A79F CRC64;

Query Match 63.0%; Score 34; DB 17; Length 160;
Best Local Similarity 45.5%; Pred. NO. 49;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
| : : : | : |
DB 89 RRAQELGKKIY 99

RESULT 14
Q8JWK5
ID Q8JWK5 PRELIMINARY; PRT; 193 AA.
AC Q8JWK5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Hypothetical protein NMA0330.
GN NMA0330.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Pratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162752; CAB83635.1; -.
InterPro; IPR002698; FTHF_c1gase.
DR Pfam; PF01812; 5-FTHF_cyc-lig; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 193 AA; 22211 MW; 7A12CE166600B27F CRC64;

Query Match 63.0%; Score 34; DB 16; Length 193;
Best Local Similarity 63.6%; Pred. NO. 60;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
| : : | : | |
DB 63 RRAQKRGAKLY 73

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RESULT 15
Q9PU79
ID Q9PU79 PRELIMINARY; PRT; 216 AA.
AC Q9PU79;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Pyruvate kinase (EC 2.7.1.40) (PK) (Fragment).
OS Crocodylus niloticus (Nile crocodile) (African crocodile).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylia; Crocodylinae; Crocodylus.
OX NCBI_TaxID=8501;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20022983; PubMed=1055283;
RA Hughes S., Zelus D., Mouchiroud D.;
RT "Warm-blooded isochore structure in Nile crocodile and turtle.";
RL Mol. Biol. Evol. 16:1521-1527(1999).
CC -!- CATALYTIC ACTIVITY: ATP + PYRUVATE -> ADP + PHOSPHOENOLPYRUVATE.
CC -!- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM (BY SIMILARITY).
CC -!- PATHWAY: FINAL STEP IN GLYCOLYSIS.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
DR EMBL; AJ011395; CAB56421.1; -.
DR HSSP; P11974; IAQF.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF00224; PK; 1.
DR PRINTS; PR01050; PYRUVTKNASE.
DR ProDom; PD001009; Pyruvate_kinase; 1.
DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
KW Glycolysis; Kinase; Magnesium; Transferase.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23509 MW; 5FCF3CEC2BDB5074 CRC64;

Query Match 63.0%; Score 34; DB 13; Length 216;
Best Local Similarity 85.7%; Pred. NO. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DIGSKLY 11
| | | | | : |
DB 45 DIGSKLY 51

Search completed: March 10, 2003, 17:00:06
Job time : 26.2759 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 15.4483 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLSDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	131	Q921W9	Q921w9 rickettsia
2	31	100.0	320	Q8VEY4	Q8vey4 brucella me
3	31	100.0	548	Q9ZDV5	Q9zdv5 rickettsia
4	31	100.0	565	Q9MBU6	Q9mbu6 chlamydia p
5	31	100.0	589	Q06967	O06967 bacillus su
6	31	100.0	589	Q921Y4	Q921y4 rickettsia
7	31	100.0	596	Q9L7X7	Q9l7x7 brucella ab
8	31	100.0	600	Q8U6S8	Q8u6s8 agrobacteri
9	31	100.0	601	Q98LY9	Q98ly9 rhizobium l
10	31	100.0	604	Q52924	Q52924 rhizobium m
11	31	100.0	606	Q9WOC5	Q9woc5 drosophila
12	31	100.0	631	Q98AT0	Q98at0 rhizobium l
13	31	100.0	947	Q08667	Q08667 plasmodium
14	31	100.0	1025	Q25693	Q25693 plasmodium
15	31	100.0	1415	Q9NG76	Q9ng76 plasmodium
16	29	93.5	612	Q962H4	Q962h4 encephalito

17	29	93.5	1552	5	Q9VUE8
18	28	90.3	43	3	Q9URF0
19	28	90.3	85	2	Q54733
20	28	90.3	111	3	Q05453
21	28	90.3	149	5	Q9YOC3
22	28	90.3	255	10	Q9FFM7
23	28	90.3	289	5	Q9VGV0
24	28	90.3	301	5	Q9NKY3
25	28	90.3	327	2	O30552
26	28	90.3	327	16	O26096
27	28	90.3	327	16	Q9ZJ34
28	28	90.3	351	2	Q93K83
29	28	90.3	387	16	Q9ACT1
30	28	90.3	469	4	O14573
31	28	90.3	534	16	P73533
32	28	90.3	546	16	O8Y2A7
33	28	90.3	564	16	O8REL9
34	28	90.3	565	5	Q9BL17
35	28	90.3	571	2	O54121
36	28	90.3	575	16	Q9Z7A1
37	28	90.3	578	16	O8Y3T6
38	28	90.3	583	2	O32748
39	28	90.3	583	16	Q8RFT9
40	28	90.3	587	5	Q9U7F4
41	28	90.3	587	16	Q99YA5
42	28	90.3	587	16	O8U754
43	28	90.3	588	16	O9RRV6
44	28	90.3	592	16	O8Y258
45	28	90.3			

ALIGNMENTS

RESULT 1

Q921W9 PRELIMINARY; PRT; 131 AA.
AC Q921W9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN RC0301.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AF008596; AAL02839.1; ;
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 131 AA; 14753 MW; C8484BCCA612872D CRC64;

Query Match 100.0%; Score 31; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

QY 1 ATSSLSDS 7
|||||||
Db 62 ATSSLSDS 68

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RESULT 2
Q8YEY4 PRELIMINARY; PRT; 320 AA.
AC Q8YEY4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ABC transporter ATP-binding protein.
GN BME11743.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RA "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009607; AAL52924.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Complete proteome.
SQ SEQUENCE 320 AA; 35768 MW; 95DBAB38430A2C01 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 320;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 235 ATSSLS 241

RESULT 3
Q9ZDV5 PRELIMINARY; PRT; 548 AA.
AC Q9ZDV5;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ABC transporter ATP-binding protein (ABCT3).
GN RP214.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.S., Winkler H.H., Kurland C.G.;
RA "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS)
DR EMBL; AJ235270; CAAL4677.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportrTM.
DR InterPro; IPR003439; ABC_transportr.

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DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 548 AA; 62589 MW; B4ED4E7F9D53EDC9 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 548;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 470 ATSSLS 476

RESULT 4
Q9MBU6 PRELIMINARY; PRT; 565 AA.
AC Q9MBU6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Structural protein.
GN VPI.
OS Chlamydia phage 2.
OC Viruses; ssDNA viruses; Microviridae; Chlamydiaviridae.
OX NCBI_TaxID=105154;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=20193783; PubMed=10729119;
RA Liu B., Everson J.S., Fane B., Giannikopoulou P., Vretou E.,
RA Lambden P.R., Clarke I.N.;
RA "Molecular characterisation of a bacteriophage (Chp2) from Chlamydia
RT psittaci."
RL J. Virol. 74:3464-3469(2000).
DR EMBL; AJ270057; CAB85589.1; -.
SQ SEQUENCE 565 AA; 63538 MW; 670485CDC2A94932 CRC64;

Query Match 100.0%; Score 31; DB 9; Length 565;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 497 ATSSLS 503

RESULT 5
O06967 PRELIMINARY; PRT; 589 AA.
AC O06967;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein yvcc.
GN YVCC.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Denizot F.C.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;

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RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N.G., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidis A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokini M., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RT Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
DR EMBL; Z94043; CAB08051.1; -.
DR EMBL; Z99121; CAB15487.1; -.
DR HSSP; P13569; 1NED.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportrTM.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Hypothetical protein; Transport; Complete proteome.
SQ SEQUENCE 589 AA; 64519 MW; 8A15163B5698DA08 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 589;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 505 ATSSLS 511

RESULT 6
Q921Y4 PRELIMINARY; PRT; 589 AA.
AC Q921Y4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding protein.
GN ABC23 OR RC0286.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.

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OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sanson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008594; AA02824.1; -.
DR InterPro; IPR001140; ABCtransportrTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR PRODOM; PD000006; ABC_transportr; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 589 AA; 67062 MW; 568DDCACC02B62773 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 589;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 511 ATSSLS 517

RESULT 7
Q9L7X7 PRELIMINARY; PRT; 596 AA.
AC Q9L7X7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC transporter protein (fragment).
GN EXSA.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S19;
RA Freitas D.A., Miyoshi A., Oliveira S.C., Azevedo V.;
RT "Cloning and sequence analysis of the exsA gene encoding an ABC
RT transporter protein from Brucella abortus.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218367; AAF64672.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportrTM.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR PRODOM; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
KW ATP-binding.
FT NON_TER
SQ SEQUENCE 596 AA; 65461 MW; 3CD7B48078C419C3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 596;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLS 7
Db 510 ATSSLS 516

RESULT 8
Q8U6S8 PRELIMINARY; PRT; 600 AA.
ID Q8U6S8

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AC Q8U6S8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE ABC transporter, nucleotide binding/ATPase protein.
 GN EXSA OR ATU4728 OR AGR_L_309.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Hourollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Quemello K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL; AE009401; AAL45522.1; -;
 DR EMBL; AE008213; AAK88722.1; -;
 KW Complete proteome.
 SQ SEQUENCE 600 AA; 65880 MW; B74D36107BD753E9 CRC64;
 Query Match 100.0%; Score 31; DB 16; Length 600;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSLDS 7
 Db 517 ATSSLDS 523
 RESULT 9
 Q98LY9
 ID Q98LY9 PRELIMINARY; PRT; 601 AA.
 AC Q98LY9;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DE ABC transporter, nucleotide binding/ATPase protein.
 GN MLL0815.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=MAFF303099;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP002995; BAB48324.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABCtransprtm.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 601 AA; 65926 MW; 21FE62D90E6D585A CRC64;
 Query Match 100.0%; Score 31; DB 16; Length 601;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSLDS 7
 Db 518 ATSSLDS 524
 RESULT 10
 Q52924
 ID Q52924 PRELIMINARY; PRT; 604 AA.
 AC Q52924;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE EXSA protein (MSBA-like SACCHARIDE EXPORTING ABC transporter protein,
 DE CONSISTING OF ATP-binding and permease domains).
 GN EXSA OR RB1064 OR SMB20941.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid psymb (megaplasmid 2).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=RCR2011 / SU47;
 RA Becker A., Kuester H., Niehaus K., Puehler A.;
 RT "Extension of the Rhizobium meliloti succinoglycan biosynthesis gene
 RT cluster: identification of the exsa gene encoding an ABC transporter
 RT protein, and the exsB gene which probably codes for a regulator of
 RT succinoglycan biosynthesis.";
 RL Mol. Gen. Genet. 249:487-497(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RCR2011 / SU47;
 RA Becker A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RCR2011 / SU47;
 RA York G.M., Walker G.C.;
 RL Mol. Microbiol. 25:117-134(1997).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021; PLASMID=PSYMB (MEGAPLASMID 2);
 RX MEDLINE=21396508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Gouzy J.,
 RA Vorhoelter F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
 RA Golding B., Puehler A.;
 RT "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 CC -1- SIMILARITY: BELONGS TO THE ABC_TRANSPORTER FAMILY.
 DR EMBL; Z50189; CAA90568.1; -;
 DR EMBL; AJ225561; CAA12529.1; -;

DR EMBL; AL603645; CAC49464.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABCtransprtrM.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport; plasmid; Complete proteome.
 SQ SEQUENCE 604 AA; 66094 MW; 2C759C1FF0BAB12A CRC64;

Query Match 100.0%; Score 31; DB 16; Length 604;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7
 Db 518 ATSSLS 524
 |||||

RESULT 11
 Q9W0C5 PRELIMINARY; PRT; 606 AA.
 ID Q9W0C5
 AC Q9W0C5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE CG7955 protein (GH20617P).
 GN CG7955
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Foster C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Sampson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AE003472; AAF47525.1; -;
 DR EMBL; AY051556; AAK92980.1; -;
 DR FlyBase; FBgn0035244; CG7955.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABCtransprtrM.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 606 AA; 66104 MW; 76C80500A1B62327 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 606;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7
 Db 511 ATSSLS 517
 |||||

RESULT 12
 Q98AT0
 ID Q98AT0 PRELIMINARY; PRT; 631 AA.
 AC Q98AT0;
 DT 01-OCT-2001 (TReMBLrel. 18, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE ABC transporter, ATP-binding protein, ExsA.
 GN MLR5867.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003007; BAB52242.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABCtransprtrM.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 631 AA; 69489 MW; A7DAEB1F457A6985 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 631;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7
|||||
Db 543 ATSSLS 549

RESULT 13

Q08667 ID Q08667 PRELIMINARY; PRT; 947 AA.
AC Q08667;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Transport protein.
GN MDR2.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB3/W2;
RX MEDLINE=94158979; PubMed=8114829;
RA Zalis M.G., Wilson C.M., Zhang Y., Wirth D.F.;
RT "Characterization of the pfmdr2 gene for Plasmodium falciparum
[published erratum appears in Mol Biochem Parasitol 1994
Feb;63(2):311].";
RT Mol. Biochem. Parasitol. 62:83-92(1993).
RN [2]

RN SEQUENCE FROM N.A.

RC STRAIN=HB3/W2;
RX MEDLINE=94277156; PubMed=7911976;
RA Zalis M.G., Wilson C.M., Zhang Y., Wirth D.F.;
RT "Characterization of the pfmdr2 gene for Plasmodium falciparum.";
RN Mol. Biochem. Parasitol. 63:311-311(1994).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; L13381; AAA61983.1; -;
DR HSSP; P13569; INBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportrTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 947 AA; 110246 MW; 5D7B1D39515C4C71 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 947;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7
|||||
Db 849 ATSSLS 855

RESULT 14

Q25693 ID Q25693 PRELIMINARY; PRT; 1025 AA.
AC Q25693;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pfmdr2 protein.
GN PFMDR2.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D10;
RX MEDLINE=94333528; PubMed=7914495;
RA Rubio J.P., Cowman A.F.;
RT "Plasmodium falciparum: the pfmdr2 protein is not overexpressed in
RT chloroquine-resistant isolates of the malaria parasite.";
RL Exp. Parasitol. 79:137-147(1994).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; U04640; AAA21513.1; -;
DR HSSP; P13569; INBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportrTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport.
SQ SEQUENCE 1025 AA; 119152 MW; 91AF3BD8916D520D CRC64;

Query Match 100.0%; Score 31; DB 5; Length 1025;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7
|||||
Db 851 ATSSLS 857

RESULT 15

Q9NG76 ID Q9NG76 PRELIMINARY; PRT; 1415 AA.
AC Q9NG76;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Multidrug resistance protein Pgh1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCCL/HN;
RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RT "Mutations in the multidrug resistance (MDR) gene of Plasmodium
RT falciparum isolate FCCL/HN".
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AF258325; AAF71750.1; -;
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportrTM.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transportr; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
KW ATP-binding; Transport.
SQ SEQUENCE 1415 AA; 161797 MW; 8C6381117940427 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 1415;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7
|||||
Db 1334 ATSSLS 1340

Search completed: March 10, 2003, 17:00:08
Job time : 17.4483 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 19.8621 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-5

Perfect score: 47

Sequence: 1 LOYASSPYT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP-archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	47	100.0	127	11	Q925S9
2	40	85.1	312	2	Q57172
3	38	80.9	105	3	Q9Y8E0
4	38	80.9	475	10	Q9LKH7
5	35	74.5	476	17	Q8TSH3
6	35	74.5	520	3	P87105
7	35	74.5	536	17	Q97YP2
8	35	74.5	547	16	Q988I9
9	35	74.5	559	16	Q92ND1
10	35	74.5	619	16	Q8UGT5
11	35	74.5	671	3	Q94113
12	35	74.5	761	5	Q9TYU3
13	35	74.5	784	11	Q925M5
14	35	74.5	784	11	Q91XZ6
15	35	74.5	787	3	Q94096
16	35	74.5	790	3	O13304

17	35	74.5	874	3	Q96VJ2	Q96vj2 pneumocysti
18	35	74.5	897	3	Q96VJ1	Q96vj1 pneumocysti
19	35	74.5	926	3	O13305	O13305 pneumocysti
20	35	74.5	938	3	Q96VI4	Q96vi4 pneumocysti
21	35	74.5	1646	5	Q9VD85	Q9vd85 drosophila
22	35	74.5	1887	11	Q9QW67	Q9qw67 rattus sp.
23	35	74.5	1898	11	Q9EQ17	Q9eq17 mus musculu
24	35	74.5	1898	11	Q64604	Q64604 r protein-t
25	34	72.3	131	12	Q89240	Q89240 wheat dwarf
26	34	72.3	211	10	Q9M279	Q9m279 arabidopsis
27	34	72.3	461	16	Q8ZRO7	Q8zr07 arabidopsis
28	34	72.3	461	16	Q8Z815	Q8z815 salmonella
29	34	72.3	572	4	Q9UG31	Q9ug31 homo sapien
30	34	72.3	645	4	Q95928	Q95928 homo sapien
31	34	72.3	721	2	Q9L9L3	Q9l9l3 pasteurella
32	34	72.3	1254	4	Q96AY4	Q96ay4 homo sapien
33	34	72.3	1263	4	Q9UPV8	Q9upv8 homo sapien
34	33	70.2	153	12	O65346	O65346 autographa
35	33	70.2	161	10	Q9LUY0	Q9luy0 arabidopsis
36	33	70.2	223	17	Q97WP2	Q97wp2 sulfolobus
37	33	70.2	230	17	Q9Y979	Q9y979 aeropyrum p
38	33	70.2	283	3	O42871	O42871 schizosacch
39	33	70.2	312	2	Q9L796	Q9l796 porphyron
40	33	70.2	351	16	Q8ZED2	Q8zed2 yersinia pe
41	33	70.2	723	11	Q925L6	Q925l6 mus musculu
42	33	70.2	786	11	Q91Y04	Q91y04 mus musculu
43	33	70.2	792	11	Q925L3	Q925l3 mus musculu
44	33	70.2	792	11	Q91Y02	Q91y02 mus musculu
45	33	70.2	802	11	Q91Y03	Q91y03 mus musculu

ALIGNMENTS

RESULT 1

Q925S9 ID Q925S9 PRELIMINARY; PRT; 127 AA.

AC Q925S9;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Immunoglobulin light chain (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C;

RX MEDLINE=99306687; PubMed=10380019;

RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,

RA Foon K.A., Chatterjee S.K.;

RT "Construction and characterization of a chimeric fusion protein

RT consisting of an anti-idiotypic antibody mimicking a breast cancer-

RT associated antigen and the cytokine GM-CSF.";

RL Hybridoma 18-193-202(1999).

DR EMBL; AF124721; AAK55120.1;

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 1;

DR NON_TER 127; 127

SQ SEQUENCE 127 AA; 13794 MW; 13F61BEBBB981FA5 CRC64;

Query Match 100.0%; Score 47; DB 11; Length 127;

Best Local Similarity 100.0%; Pred. No. 0.081;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOYASSPYT 9

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Db 109 LOYASSPYT 117

RESULT 2

Q57172

```
ID Q57172 PRELIMINARY; PRT; 312 AA.
AC Q57172;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Homology to HYDROLASES.
GN ESTB.
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=95400495; PubMed=7670642;
RA Geissdoerfer W., Frosch C.S., Haspel G., Ehart S., Hillen W.;
RT "Two genes encoding proteins with similarities to rubredoxin and
RT rubredoxin reductase are required for conversion of dodecane to lauric
RT acid in Acinetobacter calcoaceticus ADP1.";
RL Microbiology 141:1425-1432(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RA Geissdoerfer W.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RA Geissdoerfer W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=BD413;
RA Kok R.G., Bart A., Hellingwerf K.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; 246863; CAA86927.1;
DR EMBL; X88895; CAA61351.1;
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
KW Hydrolase.
SQ SEQUENCE 312 AA; 34680 MW; 14E020BA7654D905 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 312;
Best Local Similarity 77.8%; Pred. No. 5.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
Db 5 LOFSSSPYT 13

RESULT 3
QY8E0 PRELIMINARY; PRT; 105 AA.
AC QY8E0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Subtilisin-like serine protease (Fragment).
GN PRT1.
OS Pneumocystis carinii f. sp. rattii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=38082;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97388577; PubMed=9245811;
RA Lugli E.B., Allen A.G., Wakefield A.E.;
RT "A Pneumocystis carinii multi-gene family with homology to subtilisin-
RT like serine proteases.";
RL Microbiology 143:2223-2236(1997).
RN [2]
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RP SEQUENCE FROM N.A.
RA Lugli E.B., Bampton E.T., Ferguson D.J.P., Wakefield A.E.;
RT "Cell Surface protease PRT1 identified in the fungal pathogen
RT Pneumocystis carinii.";
RL Mol. Microbiol. 31:0-0(1999).
DR EMBL; AF126252; AAD39924.1; -.
DR MEROPS; S08.011; -.
DR InterPro; IPR00209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.
KW Protease.
FT NON_TER 1 1
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11163 MW; 8C00CE05BE61BAAB CRC64;

Query Match 80.9%; Score 38; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
Db 51 YASSPYT 57

RESULT 4
Q9LKB7 PRELIMINARY; PRT; 475 AA.
AC Q9LKB7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gb|AAB82637.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000370; BAA97050.1; -.
SQ SEQUENCE 475 AA; 54738 MW; 39DAE2288B590701 CRC64;

Query Match 80.9%; Score 38; DB 10; Length 475;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYASSPY 8
Db 106 LOYAQSPY 113

RESULT 5
Q8TSH3 PRELIMINARY; PRT; 476 AA.
AC Q8TSH3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ss-DNA-specific exonuclease.
GN RECJ OR MA0823.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
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OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010744; AA004262.1; -.
KW Exonuclease; Complete proteome.
SQ SEQUENCE 476 AA; 52740 MW; 62428E5283AE8AA0 CRC64;

Query Match 74.5%; Score 35; DB 17; Length 476;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYASSPY 8
Db 212 LOYSSDPY 219
||:|||||

RESULT 6
P87105 PRELIMINARY; PRT; 520 AA.
AC P87105;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Subtilisin-like protease 3 (Fragment).
GN SUBP3.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170707; PubMed=9508440;
RA Wada M., Nakamura Y.;
RT "cDNA cloning and overexpression of cell surface subtilisin-like
RT proteases (SSP) of Pneumocystis carinii.";
RL J. Eukaryot. Microbiol. 44:54S-54S(1997).
DR EMBL; AB003499; BAAL973.1; -.
DR HSP; P00782; IYJB.
DR MEROPS; S08.011; -.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
KW Protease.
FT NON_TER 1
FT NON_TER 520
FT NON_TER 520
SQ SEQUENCE 520 AA; 57529 MW; FD10F82E9E8B93D3 CRC64;

Query Match 74.5%; Score 35; DB 3; Length 520;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9

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Db 172 YANSPYT 178
||:|||||

RESULT 7
Q97YP2 PRELIMINARY; PRT; 536 AA.
AC Q97YP2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Oligo/dipeptide transport, permease protein (dppc-2).
GN DPPC-2 OR SSO1283.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aveyez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA de Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Koza C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duquet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006742; AAK41520.1; -.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBR; 1.
KW Complete proteome.
SQ SEQUENCE 536 AA; 59322 MW; 134A43BD8C60D3EF CRC64;

Query Match 74.5%; Score 35; DB 17; Length 536;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPY 8
Db 47 QYAASPY 53
||:|||||

RESULT 8
Q98819 PRELIMINARY; PRT; 547 AA.
AC Q98819;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein ml16723.
GN MLL6723.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida I., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003010; BAB52961.1; -.
KW Hypothetical protein; Complete proteome.

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SQ SEQUENCE 547 AA; 60809 MW; 89BBF8D4D2B88499 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 547;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9

Db 450 LOYASDPVT 458

RESULT 9

Q92ND1

ID Q92ND1 PRELIMINARY; PRT; 559 AA.

AC Q92ND1; (11) | | | | |
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical transmembrane protein SMC01665.
GN R02277 OR SMC01665.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetalle D., Puehler A., Purnelle B., Rampsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021".
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591790; CAC46856.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 559 AA; 61358 MW; 1663C17276640F4F CRC64;

Query Match 74.5%; Score 35; DB 16; Length 559;
Best Local Similarity 77.8%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9

Db 463 LOYASDPVT 471

RESULT 10

Q8UGT5

ID Q8UGT5 PRELIMINARY; PRT; 619 AA.

AC Q8UGT5; (11) | | | | |
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical protein Atu0950.
GN ATU0950 OR AGR_C.1734.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Ourullo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009059; AAL41964.1; -.
DR EMBL; AE008025; AAK86755.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 619 AA; 68652 MW; EE66684BCB04A2C9 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 619;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9

Db 517 LOYASDPVT 525

RESULT 11

O94113

ID O94113 PRELIMINARY; PRT; 671 AA.

AC O94113; (11) | | | | |
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Kexin (Fragment).
OS KEXIN.
GN Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX Russian D.A., Andrawis-Sorial V., Angus C.W., Kovacs J.A.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U82999; AAD00541.1; -.
DR MEROPS; S08.011; -.
DR InterPro; IPR002029; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR InterPro; IPR002965; P_rich_extensn.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 671 AA; 74049 MW; BAC4A164EC007C2E CRC64;

Query Match 74.5%; Score 35; DB 3; Length 671;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9

Db 177 YANSPYT 183

RESULT 12

Q9TYU3
 ID Q9TYU3 PRELIMINARY; PRT; 761 AA.
 AC Q9TYU3;
 DT 01-MAY-2000 (TremBLrel. 13, Created)
 DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Hypothetical 88.4 kba protein.
 GN VC5.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Tin-wollam A.M.; Wohldmann P.;
 RT "The sequence of C. elegans cosmid VC5.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 DR EMBL; AF106581; AAC78212.1; -.
 DR HSSP; P20393; IAGY.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001628; ZnfC4steroid.
 DR Pfam; PF00104; hormone_rec; 2.
 DR Pfam; PF00105; zf-C4; 2.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; ZnfC4steroid; 2.
 DR SMART; SM00430; HOL1; 2.
 DR SMART; SM00399; ZnfC4; 2.
 KW DNA-binding; Hypothetical protein; Nuclear protein; Receptor;
 KW Transcription regulation; Zinc-finger.
 SQ SEQUENCE 761 AA; 88417 MW; FFD60271DF28ED2D CRC64;

Query Match 74.5%; Score 35; DB 5; Length 761;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
 I:|||||
 Db 99 YSSPYT 105

RESULT 13
 Q925M5 PRELIMINARY; PRT; 784 AA.
 ID Q925M5
 AC Q925M5;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Protocadherin-betaD.
 DE Protocadherin-betaD.
 GN PCDHB4 OR PCDHB5A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21223055; PubMed=11322959;

RA Vanhalst K., Kools P., Vanden Eynde E., van Roy F.;
 RT "The human and murine protocadherin-beta one-exon gene families show
 RT high evolutionary conservation, despite the difference in gene
 RT number.";
 RL FEBS Lett. 495:120-125(2001).
 CC -!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
 DR EMBL; AF326297; AAK53222.1; -.
 DR MGD; MGI:2136738; Pcdhb4.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; cadherin; 5.
 DR PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
 DR PROSITE; PS0268; CADHERIN_2; 6.
 KW Calcium-binding; Cell adhesion; Glycoprotein.
 SQ SEQUENCE 784 AA; 85819 MW; 9C0524BCF3A81F45 CRC64;

Query Match 74.5%; Score 35; DB 11; Length 784;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYASSPYT 9
 I:|||||
 Db 564 LONASAPYT 572

RESULT 14
 Q91XZ6 PRELIMINARY; PRT; 784 AA.
 ID Q91XZ6
 AC Q91XZ6;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Protocadherin beta 4.
 GN PCDHB4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=99308636; PubMed=10380929;
 RA Wu Q., Maniatis T.;
 RT "A striking organization of a large family of human neural cadherin-
 RT like cell adhesion genes.";
 RL Cell 97:779-790(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=20202599; PubMed=10716726;
 RA Wu Q., Maniatis T.;
 RT "Large exons encoding multiple ectodomains are a characteristic
 RT feature of protocadherin genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=21154914; PubMed=11230163;
 RA Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz J.,
 RA Dickson M., Noonan J.P., Zhang M.O., Myers R.M., Maniatis T.;
 RT "Comparative dna sequence analysis of mouse and human protocadherin
 RT gene clusters.";
 RL Genome Res. 11:389-404(2001).
 CC -!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
 DR EMBL; AY013786; AAK26075.1; -.
 DR MGD; MGI:2136738; Pcdhb4.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; cadherin; 5.
 DR PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
 DR PROSITE; PS0268; CADHERIN_2; 6.
 KW Calcium-binding; Cell adhesion; Glycoprotein.
 SQ SEQUENCE 784 AA; 85778 MW; 13A0337BBAAE26FC CRC64;

Query Match 74.5%; Score 35; DB 11; Length 784;

Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYASSPYT 9
|||
Db 564 LONASAPYT 572

RESULT 15

O94096 PRELIMINARY; PRT; 787 AA.
AC O94096;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Kexin.
GN KEX.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RA Russian D.A., Edman J.C., Angus C.W., Sorial V., Turner R.,
RA Kovacs J.A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U62910; AAD00101.1; -
DR HSP; P00782; 2SBT.
DR MEROPS: S08.011; -
DR InterPro; IPR00209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR InterPro; IPR002965; P-rich_extensn.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
SQ SEQUENCE 787 AA; 88916 MW; 2C9F572BF636632F CRC64;

Query Match 74.5%; Score 35; DB 3; Length 787;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
|||
Db 362 YANSPYT 368

Search completed: March 10, 2003, 17:00:10
Job time : 21.8621 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 6.82759 seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	42	77.8	130	1 KV5G_MOUSE	P01639 mus musculus
2	37	68.5	234	1 YF52_YEAST	P36018 saccharomyc
3	37	68.5	527	1 MET3_CANAL	Q9Y872 candida alb
4	34	63.0	251	1 R33A_SCHPO	Q09781 schizosacch
5	34	63.0	494	1 ICSB_SHIFL	P33546 shigella fl
6	34	63.0	650	1 DNAK_BURPS	O68191 burkholderi
7	34	63.0	876	1 SVV_MYCTU	O53175 mycobacteri
8	34	63.0	920	1 C04_BOVIN	P01030 bos taurus
9	33	61.1	115	1 KV5L_MOUSE	P01642 mus musculus
10	33	61.1	237	1 YW9A_YEAST	Q04902 saccharomyc
11	33	61.1	322	1 CGM2_SCHPO	P36613 schizosacch
12	33	61.1	415	1 CSCB_ECOLI	P30000 escherichia
13	33	61.1	529	1 KPYK_CHICK	P00548 gallus gall
14	33	61.1	641	1 DNAK_METSS	O92fc6 methylovoru
15	33	61.1	656	1 DNAK_ALCEU	O33522 alcaligenes
16	33	61.1	663	1 MNEL_YEAST	P24720 saccharomyc
17	32	59.3	103	1 CHLB_SELMO	P37856 sellaginella
18	32	59.3	162	1 CBP6_YEAST	P07253 saccharomyc
19	32	59.3	183	1 YH96_ARCFU	O28478 archaeoglob
20	32	59.3	261	1 R33A_ORYSA	P49397 oryza sativ
21	32	59.3	335	1 GCP_AQUAE	O66986 aquifex aeo
22	32	59.3	388	1 SUCC_SALTY	Q8xep0 salmonella
23	32	59.3	403	1 YNR5_YEAST	P53883 saccharomyc
24	32	59.3	404	1 TRPB_METJA	Q60179 methanococc
25	32	59.3	512	1 GUAA_CHLMU	O9pkm3 chlamydia m
26	32	59.3	530	1 KPYL_RABIT	P11974 oryctolagus
27	32	59.3	530	1 KPY2_RABIT	O18919 oryctolagus
28	32	59.3	650	1 DNAK_BURCE	P42373 burkholderi
29	32	59.3	715	1 GRE4_CHLTR	O48464 chlamydia t
30	32	59.3	1229	1 KPBA_DROME	Q9w391 drosophila
31	31	57.4	108	1 KV5K_MOUSE	P01644 mus musculus
32	31	57.4	108	1 KV5L_MOUSE	P01645 mus musculus
33	31	57.4	108	1 KV5M_MOUSE	P01646 mus musculus

34	31	57.4	108	1 KV5N_MOUSE	P01647 mus musculus
35	31	57.4	108	1 KV5O_MOUSE	P01648 mus musculus
36	31	57.4	108	1 KV5P_MOUSE	P01649 mus musculus
37	31	57.4	115	1 KV5F_MOUSE	P01638 mus musculus
38	31	57.4	128	1 KV5E_MOUSE	P01637 mus musculus
39	31	57.4	169	1 SNFB_YEAST	P38956 saccharomyc
40	31	57.4	188	1 Y101_UREPA	Q9pr43 ureaplasma
41	31	57.4	251	1 RS3B_SCHPO	O94438 schizosacch
42	31	57.4	275	1 YMA9_CAEEL	P34454 caenorhabdi
43	31	57.4	293	1 YNEJ_ECOLI	P77309 escherichia
44	31	57.4	385	1 GBAL_SOYBN	P49084 glycine max
45	31	57.4	399	1 Y538_STRPY	Q9a028 streptococc

ALIGNMENTS

RESULT 1
KV5G_MOUSE
ID KV5G_MOUSE STANDARD; PRT: 130 AA.
AC P01639; P01640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 41 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79221900; PubMed=111146;
RA Seidman J.G., Max E.E., Leder P.;
RT "A kappa-immunoglobulin gene is formed by site-specific recombination
RT without further somatic mutation.;
RL Nature 280:370-375(1979).
RN [2]
RP SEQUENCE OF 1-33.
RX MEDLINE=77148916; PubMed=403522;
RA Burstein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
RT precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT chains.;
RN [3]
RP SEQUENCE OF 23-130.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.;
RT "Mechanism of antibody synthesis: size differences between mouse
RT kappa chains.;
RL Science 155:465-467(1967).
CC -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
CC SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01922; KVM5M4.
DR HSP; P01607; IREL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region; Signal; Bence-Jones protein.
FT SIGNAL 1 22
FT CHAIN 23 130 IG KAPPA CHAIN V-V REGION MOPC 41.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT VARIANT 1 2 MISSING (IN 25% OF THE MOLECULES).
FT NON_TER 130 130

SQ SEQUENCE 130 AA; 14311 MW; 5E5F0FE71D5F1BEC CRC64;
 Query Match 77.8%; Score 42; DB 1; Length 130;
 Best Local Similarity 90.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
 |||||
 DB 46 RASQDIGSSL 55

RESULT 2
 ID YP52_YEAST STANDARD; PRT; 234 AA.
 AC P36018;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GTP-binding protein YP52.
 GN YPT52 OR YKR014C OR YK112.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94216368; PubMed=8163546;
 RA Singer-Krueger B., Stenmark H., Dueterhoeft A., Philippsen P.,
 RA Yoo J.-S., Gallwitz D., Zerial M.;
 RT "Role of three rab5-like GTPases, Ypt51p, Ypt52p, and Ypt53p, in the
 RT endocytic and vacuolar protein sorting pathways of yeast.";
 RL J. Cell Biol. 125:283-298(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RA Dueterhoeft A., Moestl D., Poehlmann R., Philippsen P.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR TRANSPORT IN THE ENDOCYTIC PATHWAY AND
 CC POSSIBLE SORTING OF THE VACUOLAR HYDROLASES SUGGESTING A
 CC PATHWAY.
 CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
 CC RAB5 HOMOLOG.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X76174; CAA53770.1; -
 CC EMBL; Z28239; CAA82086.1; -
 CC PIR; S38083; S38083.
 CC HSP; P36017; ILEK0.
 CC SGD; S0001722; YPT52.
 CC InterPro; IPR003579; GTPase_Rab.
 CC InterPro; IPR001806; Ras_trnsmfmg.
 CC InterPro; IPR005225; Small_GTP.
 CC Pfam; PF00071; ras; 1.
 CC PRINTS; PR00449; RASTRNSFRMG.
 CC SMART; SM00175; RAB; 1.
 CC TIGRFAMS; TIGR00231; small_gtp; 1.
 KW Protein transport; GTP-binding; Lipoprotein; Prenylation.
 FT NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 66 70 GTP (BY SIMILARITY).
 FT NP_BIND 111 114 GTP (BY SIMILARITY).
 FT LIPID 232 232 GERANYL-GERANYL (BY SIMILARITY).
 FT LIPID 233 233 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 234 AA; 26132 MW; 34AB2FEE38697261 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 234;
 Best Local Similarity 90.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 87.5%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QDIGSKLY 11
 |||||
 DB 187 QDIGEKLY 194

RESULT 3
 ID MET3_CANAL STANDARD; PRT; 527 AA.
 AC QY872;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylylate
 DE transferase) (SAT) (ATP-sulfurylase).
 GN MET3.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=124;
 RX MEDLINE=20032052; PubMed=10564518;
 RA Care R.S., Trevethick J., Binley K.M., Sudbery P.E.;
 RT "The MET3 promoter: a new tool for Candida albicans molecular
 RT genetics";
 RL Mol. Microbiol. 34:792-798(1999).
 CC -1- CATALYTIC ACTIVITY: ATP + sulfate -> diphosphate + adenylylsulfate.
 CC -1- PATHWAY: FIRST STEP IN THE SULFATE ASSIMILATION PATHWAY THAT
 CC LEADS TO THE BIOSYNTHESIS OF METHIONINE AND CYSTEINE.
 CC -1- SIMILARITY: BELONGS TO THE SULFATE ADENYLYLTRANSFERASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF164103; AAB45374.1; -
 CC InterPro; IPR002650; ATP-sulfurylase.
 CC Pfam; PF01747; ATP-sulfurylase; 1.
 CC ProDom; PD002381; ATP-sulfurylase; 1.
 CC TIGRFAMS; TIGR00339; sotp; 1.
 KW Methionine biosynthesis; Cysteine biosynthesis; Transferase;
 KW Nucleotidyltransferase.
 SQ SEQUENCE 527 AA; 58845 MW; A986ED8B7ACE36FD CRC64;

Query Match 68.5%; Score 37; DB 1; Length 527;
 Best Local Similarity 63.6%; Pred. No. 7.4;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
 |||||
 DB 221 RAAQDIGDKAH 231

RESULT 4
 ID RS3A_SCHPO STANDARD; PRT; 251 AA.
 AC Q09781; Q09781;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S3ae-A (S1-A).
 GN RPS1A OR RPS1 OR SPAC13G6.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;

```

OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Mungall K., Murphy L., Niblett D., O'Neill C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT The genome sequence of Schizosaccharomyces pombe.;
RL Nature 415:871-880(2002).
RN [2]
RP SEQUENCE OF 1-71 FROM N.A.
RC STRAIN=968 h90.
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.O., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hiraoka Y.;
RT "Large-scale screening of intracellular protein localization in living
RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
CC -!- MISCELLANEOUS: THERE ARE TWO GENES FOR S1 IN S.POMBE.
CC -!- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL; Z54308; CAA91095.1; -.
CC EMBL; AB027994; BAA87298.1; -.
CC InterPro; IPR001593; Ribosomal_S3AE.
CC Pfam; PF01015; Ribosomal_S3AE; 1.
CC ProDom; PD003035; Ribosomal_S3AE; 1.
CC PROSITE; PS01191; RIBOSOMAL_S3AE; 1.
CC KEGG Ribosomal protein; Multigene family.
CC INIT_MET 0 BY SIMILARITY.
SQ SEQUENCE 251 AA; 28357 MW; 2A254B63415A9B98 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 251;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 SODIGSKL 10
DB 234 SODVGSKV 241
|||||:
|||||:

RESULT 5
ICSB_SHIFL
NCBI_TaxID=4896;
PRT; 494 AA.
STANDARD;
PRT; 494 AA.
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Intercellular spread protein.
ICSB.
Shigella flexneri.
Plasmid 210 kb invasion pWR100.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Shigella.
NCBI_TaxID=623;
[1]
SEQUENCE FROM N.A.
STRAIN=M90T / Serotype 5;
MEDLINE=92356824; PubMed=1495389;
Allaoui A., Mounier J., Prevost M.-C., Sansonetti P.J., Parsot C.;
"icSB: a Shigella flexneri virulence gene necessary for the lysis of
protrusions during intercellular spread.";
Mol. Microbiol. 6:1605-1616(1992).
[2]
SEQUENCE OF 1-19 FROM N.A.
STRAIN=M90T / Serotype 5;
MEDLINE=92339268; PubMed=8478058;
Allaoui A., Menard R., Sansonetti P.J., Parsot C.;
"Characterization of the Shigella flexneri ipgd and ipgf genes, which
are located in the proximal part of the mxi locus.";
Infect. Immun. 61:1707-1714(1993).
-!- FUNCTION: NECESSARY FOR THE LYSIS OF PROTRUSIONS DURING
INTERCELLULAR SPREAD.
-!- SUBCELLULAR LOCATION: PERIPLASMIC. THE PERIPLASM MAY REPRESENT
A RESERVOIR FOR THE PROTEIN, IT WOULD BE RELEASED AT A LATER
STAGE DURING THE INFECTION CYCLE.
-----
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CC -----
CC EMBL; M86530; AAD15221.1; -.
CC PIR; S22687; S22687.
CC Plasmid; Virulence; Periplasmic.
SQ SEQUENCE 494 AA; 56323 MW; DC975ECB76FB57BB CRC64;

Query Match 63.0%; Score 34; DB 1; Length 494;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 SODIGSKLY 11
DB 467 SPDLGTLKY 475
|||||:
|||||:

RESULT 6
DNAK_BURPS
STANDARD;
PRT; 650 AA.
068191;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
protein) (HSP70).
DNAK.
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
NCBI_TaxID=28450;
[1]
SEQUENCE FROM N.A.
STRAIN=ATCC 23343;

```

RA See L.H., Yap E.H., Yap E.P.H.;
 RT "Isolation and sequencing of the heat shock protein 70 (hsp70/dnak)
 gene in Burkholderia pseudomallei";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
 CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF016711; AAC15473.1; -
 CC HSP; P04475; IDG4
 CC InterPro: IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70; 1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC ProDom; PD000089; Hsp70; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 CC Chaperone; ATP-binding; Heat shock; Phosphorylation.
 KW MOD_RES 200 200 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT SEQUENCE 650 AA; 69735 MW; BE46330B6DE174D0 CRC64;
 SQ
 Query Match 63.0%; Score 34; DB 1; Length 650;
 Best Local Similarity 60.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ASQDIGSKLY 11
 III : I I I
 Db 597 ASQKLGEKMY 606
 RESULT 7
 SYV_MYCTU STANDARD; PRT; 876 AA.
 ID SYV_MYCTU STANDARD; PRT; 876 AA.
 AC OS3175;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
 GN VALS OR RV2448C OR MT2524 OR MTV008.04C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton M., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence."
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) -> AMP + diphosphate
 CC + L-valyl-tRNA(Val).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AL021246; CAA16025.1; -
 CC HSP; AE007089; AAK46823.1; -
 CC TIGR; P96142; IGAX.
 CC TuberculList; RV2448c; -
 CC InterPro: IPR002300; tRNA-synt_1a.
 CC InterPro: IPR001412; tRNA-synt_1.
 CC InterPro: IPR002303; tRNA-synt_val.
 CC Pfam; PF00133; tRNA-synt_1; 1.
 CC PRINTS; PR00986; TRNASYNTHVAL.
 CC TIGRFAMS; TIGR00422; vals; 1.
 CC PROSITE; PS00178; AA-TRNA-LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 43 53 "HIGH" REGION.
 FT SITE 530 534 "KMSK" REGION.
 FT BINDING 533 533 ATP (BY SIMILARITY).
 SQ SEQUENCE 876 AA; 97820 MW; 85C4E2C3BF76B090 CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 876;
 Best Local Similarity 54.5%; Pred. No. 52;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGSKLY 11
 III::: I I I
 Db 575 RASRNFGTKLF 585
 RESULT 8
 CO4_BOVIN STANDARD; PRT; 920 AA.
 ID CO4_BOVIN STANDARD; PRT; 920 AA.
 AC P01030; Q27993; Q27992;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Complement C4 precursor [Contains: C4a anaphylatoxin] (Fragments).
 GN C4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-77.
 RX MEDLINE=83126436; PubMed=6760852;
 RA Smith M.A., Gerrie L.M., Dunbar B., Fothergill J.E.;
 RT "Primary structure of bovine complement activation fragment C4a, the
 third anaphylatoxin. Purification and complete amino acid sequence.";
 RL Biochem. J. 207:253-260(1982).
 RN [2]
 RP SEQUENCE OF 78-920 FROM N.A.
 RC TISSUE=Liver;
 RA Groth D.M.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE

CC CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY
 CC ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
 CC ANAPHYLATOXIN.
 CC -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4.
 CC C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES.
 CC -!- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR
 CC AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
 CC OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
 CC -!- MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
 CC PROTEIN.
 CC -!- SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.
 CC -!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U16750; AAA52751.1; -;
 CC EMBL; U16749; AAA52750.1; -;
 CC PIR; A01265; C4BOAT.
 CC HSSP; P01031; ICFA.
 CC InterPro; IPR000020; Anaphylatoxin.
 CC InterPro; IPR001840; Anaphylatoxn.
 CC InterPro; IPR001599; MacroglobulinA2.
 CC InterPro; IPR001134; Nectrid_C.
 CC PRINTS; PR000004; ANAPHYLATOXN.
 CC ProDom; PD003264; Anaphylatoxin; 1.
 CC SMART; SM00104; ANATO; 1.
 CC PROSITE; PS00477; ALPHA_2-MACROGLOBULIN; 1.
 CC PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 CC PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 CC Complement pathway; Plasma; Glycoprotein; Sulfation;
 CC Inflammatory response.
 CC FT NON_TER 1 1
 CC FT NON_CONS 77 78
 CC FT NON_CONS 342 343
 CC FT CHAIN 1 622
 CC FT PROPEP 623 629
 CC FT CHAIN 630 920
 CC FT PEPTIDE 1 77
 CC FT DOMAIN 23 57
 CC FT DISULFID 23 49
 CC FT DISULFID 24 56
 CC FT DISULFID 37 57
 CC FT THIOLST 191 194
 CC FT MOD_RES 593 593
 CC FT MOD_RES 596 596
 CC FT MOD_RES 598 598
 CC FT CARBOHYD 504 504
 CC FT CARBOHYD 567 567
 CC SEQUENCE 920 AA; 101881 MW; 1425A0BD945F5497 CRC64;
 CC -----
 CC Query Match 63.0%; Score 34; DB 1; Length 920;
 CC Best Local Similarity 66.7%; Pred. No. 55;
 CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC QY 3 SODIGSKLY 11
 CC : : : : :
 CC Db 397 AKDIGDKLY 405
 CC -----
 CC RESULT 9
 CC KV5I_MOUSE
 CC ID KV5I_MOUSE STANDARD; PRT; 115 AA.
 CC AC P01642;
 CC DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region L7 precursor (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eumetazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81220975; PubMed=6264318;
 RA Pech M., Hochli J., Schnell H., Zachau H.G.;
 RT "Differences between germ-line and rearranged immunoglobulin V kappa
 RT coding sequences suggest a localized mutation mechanism.";
 RL Nature 291:668-670(1981).
 CC -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT
 CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
 CC LACKING RESIDUES 17-19.
 CC PIR; A01925; KVMSL7.
 CC HSSP; P80362; LWTL.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; ig; 1.
 CC SMART; SM00406; Igv; 1.
 CC Immunoglobulin V region; Signal.
 CC FT SIGNAL 1 20
 CC FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
 CC FT DOMAIN 21 43 FRAMEWORK-1.
 CC FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 CC FT DOMAIN 55 69 FRAMEWORK-2.
 CC FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 CC FT DOMAIN 77 108 FRAMEWORK-3.
 CC FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
 CC FT DISULFID 43 108 BY SIMILARITY.
 CC FT NON_TER 115 115
 CC SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;
 CC -----
 CC Query Match 61.1%; Score 33; DB 1; Length 115;
 CC Best Local Similarity 54.5%; Pred. No. 10;
 CC Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC -----
 CC QY 1 RASQDIGSKLY 11
 CC : : : : :
 CC Db 44 RASQSIGTSIH 54
 CC -----
 CC RESULT 10
 CC YM9A_YEAST
 CC ID YM9A_YEAST STANDARD; PRT; 237 AA.
 CC AC Q04902;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
 CC DE Hypothetical 26.0 kDa protein in FET4-ERR1 intergenic region.
 CC GN YMR322C OR YMR924.14C.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RA Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE YMR322C/YOR391C/YPL280W (YEAST),
 CC SPAC117.06/SPAC5H10.02C/SPAC11D3.13 (S.POMBE FAMILY).
 CC -----
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CC EMBL; Z54141; CAA90840.1; -.
DR SGD; S0004941; YMR322C.
DR InterPro; IPR002818; ThiJ.
DR Pfam; PF01965; ThiJ; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 004EA3E702332905 CRC64;
-----
Query Match 61.1%; Score 33; DB 1; Length 237;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 4 QDIGSKLY 11
Db 121 QDIASKIY 128
-----
RESULT 11
CGM2_SCHPO STANDARD; PRT; 322 AA.
ID CGM2_SCHPO
AC P36613;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cyclin mcs2 (Mitotic catastrophe suppressor 2).
GN MCS2 OR SPBP16F5.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Gynonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas R., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipkovski G.V., Ussery D., Bartell B.G., Nurse P.;
RL "the genome sequence of Schizosaccharomycetes pombe.";
Nature 415:871-880(2002).
CC -!- FUNCTION: ESSENTIAL FOR PROGRESSION THROUGH THE CELL CYCLE.
CC PROBABLY INTERACTS WITH A PROTEIN KINASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
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-----
EMBL; S59895; AAB26193.1; -.
DR EMBL; AL441603; CAC08541.1; -.
DR PIR; S35380; S35380.
DR HSP; P51946; IRIXU.
DR InterPro; IPR005258; Ccl1.
DR InterPro; IPR004366; Cyclin.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR TIGRfams; TIGR00569; ccl1; 1.
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
DR Cyclin; Cell cycle; Cell division; Nuclear protein.
KW SEQUENCE 322 AA; 37673 MW; 09B8DB46563727C CRC64;
-----
Query Match 61.1%; Score 33; DB 1; Length 322;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Oy 1 RASQDIGSKLY 11
Db 266 KKAQDYGNKLY 276
-----
RESULT 12
CSCB_ECOLI STANDARD; PRT; 415 AA.
ID CSCB_ECOLI
AC P30000;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sucrose transport protein (Sucrose permease).
GN CSCB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EC3132;
RX MEDLINE=93062804; PubMed=1435727;
RA Bockmann J., Heuel H., Lengeler J.W.;
RT "Characterization of a chromosomally encoded, non-PTS metabolic
RT pathway for sucrose utilization in Escherichia coli EC3132.";
Mol. Gen. Genet. 235:22-32(1992).
CC -!- FUNCTION: PROTON SYMPORT TRANSPORT SYSTEM. HAS AN ESSENTIAL
CC ROLE IN SUCROSE METABOLISM.
CC -!- PATHWAY: SUCROSE METABOLISM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: BELONGS TO THE LACY/RAFB FAMILY OF PERMEASES.
-----
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-----
EMBL; X63740; CAA45274.1; -.
DR EMBL; X81461; CAA57217.1; -.
DR PIR; S19880; GRECS.
DR InterPro; IPR000576; Lacy_symp.
DR Pfam; PF01306; Lacy_symp; 1.
DR PRINTS; PR00174; LACY_SYMPORT.
DR TIGRfams; TIGR00882; 2A0105; 1.
DR PROSITE; PS00896; LACY_1; 1.

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DR PROSITE; PS00897; LACY_2; 1.
KW Transport; Sugar transport; Symport; Inner membrane; Transmembrane.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 48
FT TRANSMEM 49 69
FT DOMAIN 70 77
FT TRANSMEM 78 98
FT DOMAIN 99 105
FT TRANSMEM 106 126
FT DOMAIN 127 147
FT TRANSMEM 148 166
FT DOMAIN 167 189
FT TRANSMEM 190 190
FT DOMAIN 191 220
FT TRANSMEM 221 241
FT DOMAIN 242 260
FT TRANSMEM 261 281
FT DOMAIN 282 288
FT TRANSMEM 289 309
FT DOMAIN 310 312
FT TRANSMEM 313 332
FT DOMAIN 333 342
FT TRANSMEM 343 363
FT DOMAIN 364 377
FT TRANSMEM 378 398
FT DOMAIN 399 415
SQ SEQUENCE 415 AA; 46923 MW; D05BBD305B61AC22 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 415;
Best Local Similarity 55.6%; Pred. NO. 39;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SODIGSKLY 11
DB 251 SHDVGTRLY 259

RESULT 13
ID KPYK_CHICK STANDARD; PRT; 529 AA.
AC P00548;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pyruvate kinase, muscle isozyme (EC 2.7.1.40).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83221656; PubMed=6574503;
RA Lomborg N., Gilbert W.;
RT "Primary structure of chicken muscle pyruvate kinase mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3661-3665(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099332; PubMed=2981634;
RA Lomborg N., Gilbert W.;
RT "Intron/exon structure of the chicken pyruvate kinase gene.";
RL Cell 40:81-90(1985).
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
CC -!- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.
CC -!- PATHWAY: Glycolysis; final step.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- MISCELLANEOUS: THIS ACTIVITY IS REGULATED BY GLUCOSE LEVELS.
CC -!- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
-----
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-----
CC EMBL; J00903; AAA49021.1; -.
DR EMBL; M18793; AAA49020.1; JOINED.
DR EMBL; M10619; AAA49020.1; JOINED.
DR EMBL; M18788; AAA49020.1; JOINED.
DR EMBL; M18789; AAA49020.1; JOINED.
DR EMBL; M18790; AAA49020.1; JOINED.
DR EMBL; M18791; AAA49020.1; JOINED.
DR EMBL; M18792; AAA49020.1; JOINED.
DR PIR; A00659; KICHPM.
DR HSSP; P11974; LPKN.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF00224; PK_C; 1.
DR Pfam; PF02887; PK_C; 1.
DR PRINTS; PR01050; PYRUVTKINASE.
DR ProDom; PD001009; Pyruvate_kinase; 1.
DR TIGRFAMS; TIGR01064; pyruv_kin; 1.
DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
KW Transferase; Kinase; Glycolysis; Phosphorylation; Magnesium.
FT INIT_MET 0 0
FT ACT_SITE 268 268 BY SIMILARITY.
FT METAL 270 270 MAGNESIUM (POTENTIAL).
FT METAL 291 291 MAGNESIUM (POTENTIAL).
FT METAL 292 292 MAGNESIUM (POTENTIAL).
SQ SEQUENCE 529 AA; 57883 MW; 8B1907B8D31EB72F CRC64;

Query Match 61.1%; Score 33; DB 1; Length 529;
Best Local Similarity 71.4%; Pred. NO. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DIGSKLY 11
DB 167 DVGSKLY 173

RESULT 14
ID DNAK_METSS STANDARD; PRT; 641 AA.
AC Q92FC6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
DE DnaK.
GN DnaK.
OS Methylovorus sp. (strain SSI / DSM 11726).
OC Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
OC Methylovorus.
OX NCBI_TaxID=81683;
RN [1]
RP SEQUENCE FROM N.A.
RA Eom C.Y., Kim Y.M.;
RT "grpe, dnaK, and dnaJ genes of Methylovorus sp. strain SSI DSM11726.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
-----
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-----
CC EMBL; AF106835; AAC95378.1; -.
DR HSSP; P04475; IDG4.
DR InterPro; IPR001023; Hsp70.
```

Job time : 7.82759 secs

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DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 199 199 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 641 AA; 69764 MW; 7DFA5EBE144825CB CRC64;

Query Match 61.1%; Score 33; DB 1; Length 641;
Best Local Similarity 60.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
Db 594 ASQKLGEKV 603

RESULT 15
DNAME_ALCEU STANDARD; PRT; 656 AA.
AC Q33522;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
GN DNAME.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH34;
RA Talbi S., van der Lelie D.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; AJ001727; CAA04955.1; -
DR HSP; P04475; IDG4.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 200 200 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 656 AA; 71300 MW; 5C7D5D2CE22F5F97 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 656;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDIGSKLY 11
Db 595 ASQKLGEKV 604

```

Search completed: March 10, 2003, 16:57:44

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 4.34483 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	130	1 KV5G_MOUSE	P01639 mus musculus
2	31	100.0	555	1 YNS2_YEAST	P53877 saccharomyc
3	31	100.0	694	1 ABC7_MOUSE	Q61102 mus musculus
4	31	100.0	752	1 ABC7_HUMAN	O75027 homo sapien
5	31	100.0	1419	1 MDR_PLAUF	P13568 plasmodium
6	29	93.5	2404	1 SON_MOUSE	Q9qx47 mus musculus
7	29	93.5	2426	1 SON_HUMAN	P18583 homo sapien
8	28	90.3	584	1 LMRA_LACLA	O9chl8 lactococcus
9	28	90.3	584	1 LMRA_LACLC	P97046 lactococcus
10	28	90.3	586	1 Y4GM_RHISN	P55469 rhizobium s
11	28	90.3	607	1 HEPA_ANASP	P22638 anabaena sp
12	28	90.3	614	1 YA51_HAEIN	Q57180 haemophilus
13	28	90.3	685	1 MDL1_CANAL	P97998 candida alb
14	28	90.3	695	1 MDL1_YEAST	P33310 saccharomyc
15	28	90.3	698	1 CVAB_ECOLI	P22520 escherichia
16	28	90.3	698	1 MCHF_ECOLI	Q9exn5 escherichia
17	28	90.3	1280	1 MDR1_LEIEN	Q06034 leishmania
18	28	90.3	1362	1 PWD1_SCHPO	P36619 schizosacch
19	28	90.3	1444	1 DPO3_LISIN	Q92c34 listeria in
20	28	90.3	1444	1 DPO3_LISMO	Q8y7g1 listeria mo
21	27	87.1	176	1 SSB_TREPA	O83101 streptococc
22	27	87.1	237	1 LECA_DOLLA	P38662 dolichos la
23	27	87.1	302	1 KLF7_HUMAN	O75840 homo sapien
24	27	87.1	432	1 WDRL_HUMAN	Q9bv38 homo sapien
25	27	87.1	463	1 YHCL_BACSU	P54596 bacillus su
26	27	87.1	709	1 WHIT_ANOAL	Q16928 anopheles a
27	27	87.1	717	1 COMA_STRPN	Q03727 streptococc
28	27	87.1	754	1 TBP6_YEAST	P40328 saccharomyc
29	27	87.1	997	1 T257_ECOLI	P25239 escherichia
30	26	83.9	362	1 SEVE_EICDI	P10733 dictyosteli
31	26	83.9	593	1 MDLB_ECOLI	P75706 escherichia
32	26	83.9	725	1 AGAL_YEAST	P32323 saccharomyc
33	26	83.9	802	1 CIKB_RAT	Q63099 rattus norv

RESULT 1

ID	KV5G_MOUSE	STANDARD;	PRT;	130 AA.
AC	P01639; P01640;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-V region MOPC 41 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=79221900; PubMed=111146;			
RA	Seidman J.G., Max E.E., Leder P.;			
RT	"A kappa-immunoglobulin gene is formed by site-specific recombination			
RT	without further somatic mutation.";			
RL	Nature 280:370-375(1979).			
RN	[2]			
RP	SEQUENCE OF 1-33.			
RX	MEDLINE=77148916; PubMed=403522;			
RA	Burstein Y., Schechter I.;			
RT	"Amino acid sequence of the NH2-terminal extra piece segments of the			
RT	precursors of mouse immunoglobulin lambda1-type and kappa-type light			
RL	chains.";			
RN	[3]			
RP	Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).			
RX	SEQUENCE OF 23-130.			
RX	MEDLINE=67056897; PubMed=4162931;			
RA	Gray W.R., Dreyer W.J., Hood L.;			
RT	"Mechanism of antibody synthesis: size differences between mouse			
RT	kappa chains.";			
RL	Science 155:465-467(1967).			
CC	- !- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE			
CC	SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.			
CC	- !- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A01922; KVM5M4.			
DR	HSP; P01607; IREI.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; Igv; 1.			
KW	Immunoglobulin v region; Signal; Bence-Jones protein.			
FT	SIGNAL 1 22			
FT	CHAIN 23 130			
FT	IG KAPPA CHAIN V-V REGION MOPC 41.			
FT	DOMAIN 23 45			
FT	FRAMEWORK-1.			
FT	COMPLEMENTARITY-DETERMINING-1.			
FT	DOMAIN 46 56			
FT	FRAMEWORK-2.			
FT	DOMAIN 57 71			
FT	COMPLEMENTARITY-DETERMINING-2.			
FT	DOMAIN 72 78			
FT	FRAMEWORK-3.			
FT	DOMAIN 79 110			
FT	COMPLEMENTARITY-DETERMINING-3.			
FT	DOMAIN 111 119			
FT	FRAMEWORK-4.			
FT	DOMAIN 120 129			
FT	DISULFID 45 110			
FT	BY SIMILARITY.			
FT	MISSING (IN 25% OF THE MOLECULES).			
FT	VARIANT 1 2			
FT	NON_TER 130 130			

Q95167 canis famil
Q92953 homo sapien
P54706 dictyosteli
O52452 pseudanabae
Q89532 human adeno
P43241 mus musculu
P17260 homo sapien
P17260 saccharomyc
P15062 marthasteri
P18063 asterina pe
Q9J113 mus musculu
P71596 mycobacteri

ALIGNMENTS

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SQ SEQUENCE 130 AA; 14311 MW; 5EFE0FE71D5F1BEC CRC64;
Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDs 7
Db 72 ATSSLDs 78

RESULT 2
YNS2 YEAST
ID YNS2 YEAST STANDARD; PRT; 555 AA.
AC P53877;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 61.8 kDa Trp-Asp repeats containing protein in NPRI-RPS3
DE intergenic region.
GN YNL182C OR N1836.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermayer B., Piravandi E., Rinke M., Domdey H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
CC -!- SIMILARITY: TO S.POMBE SPAC13G7.08C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 271458; CAA96075.1; -
DR SGD; S0005126; YNL182C.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT REPEAT 90 133
FT REPEAT 137 176
FT REPEAT 187 234
FT REPEAT 242 383
FT REPEAT 342 383
FT REPEAT 383 400
SQ SEQUENCE 555 AA; 61773 MW; 8EED6854DF9405A6 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDs 7
Db 506 ATSSLDs 512

RESULT 3
ABC7_MOUSE
ID ABC7_MOUSE STANDARD; PRT; 694 AA.
AC Q61102;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family B, member 7, mitochondrial (ATP-
DE binding cassette transporter 7) (ABC transporter 7 protein)

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DE (Fragment).
GN ABCB7 OR ABCB7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Savary S., Allikmets R., Denizot F., Luciani M.-F., Mattei M.-G.,
RA Dean M., Chimini G.;
RL MEDLINE=97288528; PubMed=9143506;
RX STRAIN=DBA/2;
RT "Isolation and chromosomal mapping of a novel ATP-binding cassette
RT transporter conserved in mouse and human.";
RL Genomics 41:275-278(1997).
CC -!- FUNCTION: COULD BE INVOLVED IN THE TRANSPORT OF HEME FROM THE
CC MITOCHONDRIA TO THE CYTOSOL. PLAYS A CENTRAL ROLE IN THE
CC MATURATION OF CYTOSOLIC IRON-SULFUR (FE/S) CLUSTER-CONTAINING
CC PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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CC -----
DR EMBL; 043892; AAC53152.1; -
DR MGD; MGI:109533; Abcb7.
DR InterPro; IPR003593; AAA_Atpase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001140; ABCtranprtm.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transport; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transmembrane; Transport; Mitochondrion; Inner membrane.
FT NON_TER 1
FT TRANSMEM 202 222
FT TRANSMEM 233 253
FT TRANSMEM 326 346
FT NP_BIND 447 454
FT NP_BIND 454 454
SQ SEQUENCE 694 AA; 76417 MW; A7AE89EAE9AA981D CRC64;

Query Match 100.0%; Score 31; DB 1; Length 694;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDs 7
Db 577 ATSSLDs 583

RESULT 4
ABC7_HUMAN
ID ABC7_HUMAN STANDARD; PRT; 752 AA.
AC O75027; O75345; Q9UND1; Q9UP01; Q9BRE1;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family B, member 7, mitochondrial precursor
DE (ATP-binding cassette transporter 7) (ABC transporter 7 protein).
GN ABCB7 OR ABCB7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

[1] SEQUENCE FROM N.A.
RP TISSUE-Placenta;
RX MEDLINE=98284536; PubMed=9621516;
RA Shinada Y., Okuno S., Kawai A., Shinomiya H., Saito A., Suzuki M.,
RA Omori Y., Nishino N., Kanemoto N., Fujiwara T., Horie M.,
RA Takahashi E.;
RT "Cloning and chromosomal mapping of a novel ABC transporter gene
RT (hABC7), a candidate for X-linked sideroblastic anemia with
RT spinocerebellar ataxia.";
RL J. Hum. Genet. 43:115-122(1998).
[2] SEQUENCE FROM N.A.
RP TISSUE-Blood;
RX MEDLINE=98318631; PubMed=9653160;
RA Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,
RA He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,
RA Wang Y.-X., Chen S.-J., Chen Z.;
RT "Identification of genes expressed in human CD34(+) hematopoietic
RT stem/progenitor cells by expressed sequence tags and efficient full-
RT length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
[3] SEQUENCE FROM N.A., AND VARIANT ASAT MET-400.
RP MEDLINE=99214014; PubMed=10196363;
RA Allikmets R., Raskind W.H., Hutchinson A., Schueck N.D., Dean M.,
RA Koeller D.M.;
RT "Mutation of a putative mitochondrial iron transporter gene (ABC7) in
RT X-linked sideroblastic anemia and ataxia (XLSA/A).";
RL Hum. Mol. Genet. 8:743-749(1999).
[4] SEQUENCE FROM N.A., AND VARIANT ASAT LYS-433.
RP MEDLINE=20504074; PubMed=11050011;
RA Bekti S., Kispal G., Lange H., Fitzsimons E., Tolmie J., Lill R.,
RA Bishop D.F.;
RT "Human ABC7 transporter: gene structure and mutation causing X-linked
RT sideroblastic anemia with ataxia with disruption of cytosolic
RT iron-sulfur protein maturation.";
RL Blood 96:3256-3264(2000).
[5] SEQUENCE FROM N.A.
RP TISSUE-Muscle;
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
[6] SEQUENCE OF 5-752 FROM N.A.
RP MEDLINE=99098366; PubMed=9883897;
RA Csere P., Lill R., Kispal G.;
RT "Identification of a human mitochondrial ABC transporter, the
RT functional orthologue of yeast Atmlp.";
RL FEBS Lett. 441:266-270(1998).
CC -!- FUNCTION: COULD BE INVOLVED IN THE TRANSPORT OF HEME FROM THE
CC MITOCHONDRIA TO THE CYTOSOL. PLAYS A CENTRAL ROLE IN THE
CC MATURATION OF CYTOSOLIC IRON-SULFUR (FE/S) CLUSTER-CONTAINING
CC PROTEINS.
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (Potential).
CC -!- DISEASE: DEFECTS IN ABC7 ARE THE CAUSE OF X-LINKED SIDEROBLASTIC
CC ANEMIA WITH ATAXIA (ASAT). ASAT IS A RECESSIVE DISORDER
CC CHARACTERIZED BY AN INFANTILE TO EARLY CHILDHOOD ONSET OF
CC NONPROGRESSIVE CEREBELLAR ATAXIA AND MILD ANEMIA WITH HYPOCHROMIA
CC AND MICROCYTOSIS.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC
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DR EMBL; AB005289; BAA28861.1; -
DR EMBL; AF038950; AAC39865.1; -
DR EMBL; AF133659; RAD33045.1; -
DR EMBL; AF241887; AAK20173.1; -
DR EMBL; AF241872; AAK20173.1; JOINED.
DR EMBL; AF241873; AAK20173.1; JOINED.
DR EMBL; AF241874; AAK20173.1; JOINED.
DR EMBL; AF241875; AAK20173.1; JOINED.
DR EMBL; AF241876; AAK20173.1; JOINED.
DR EMBL; AF241877; AAK20173.1; JOINED.
DR EMBL; AF241878; AAK20173.1; JOINED.
DR EMBL; AF241879; AAK20173.1; JOINED.
DR EMBL; AF241880; AAK20173.1; JOINED.
DR EMBL; AF241881; AAK20173.1; JOINED.
DR EMBL; AF241882; AAK20173.1; JOINED.
DR EMBL; AF241883; AAK20173.1; JOINED.
DR EMBL; AF241884; AAK20173.1; JOINED.
DR EMBL; AF241885; AAK20173.1; JOINED.
DR EMBL; AF241886; AAK20173.1; JOINED.
DR EMBL; BC006323; AAK06323.1; -
DR EMBL; AF078777; AAD47141.1; -
DR Genew; HGNC:48; ABCB7.
DR MIM; 300135; -
DR MIM; 301310; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001140; ABCtransportrTM.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF00864; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transmembrane; Transport; Mitochondrion; Inner membrane;
KW Transit peptide; Disease mutation.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 752 ATP-BINDING CASSETTE, SUB-FAMILY B,
FT MEMBER 7.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 291 311 POTENTIAL.
FT TRANSMEM 383 403 POTENTIAL.
FT NP_BIND 505 512 ATP (POTENTIAL).
FT VARIANT 400 400 I -> M (IN ASAT).
FT FTID=VAR_009156.
FT VARIANT 433 433 E -> K (IN ASAT; IMPAIRED MATURATION OF
FT CYTOSOLIC FE/S PROTEINS).
FT FTID=VAR_012640.
FT CONFLICT 56 56 Q -> Q (IN REF. 5).
FT CONFLICT 141 141 A -> P (IN REF. 2).
FT CONFLICT 258 258 R -> K (IN REF. 1).
FT CONFLICT 271 276 LLPMF -> PLPNHV (IN REF. 2).
FT CONFLICT 281 281 V -> LV (IN REF. 2).
FT CONFLICT 290 290 G -> C (IN REF. 2).
FT CONFLICT 293 297 FALVT -> LLGN (IN REF. 2).
FT CONFLICT 315 315 R -> G (IN REF. 1).
FT CONFLICT 320 324 IEMNK -> LEIDQ (IN REF. 2).
FT CONFLICT 346 346 F -> I (IN REF. 1).
FT CONFLICT 542 542 E -> V (IN REF. 6).
SQ SEQUENCE 752 AA; 82641 MW; B1FFA57ABD24FB90 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 752;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSLDS 7
Db 635 ATSSLDS 641
RESULT 5
MDR_PLAFF STANDARD; PRT; 1419 AA.
ID MDR_PLAFF
AC P13568;
DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DR Multidrug resistance protein (Chloroquine resistance protein).
DN MDR1.
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89288297; PubMed=2701941;
RA Foote S.J., Thompson J.K., Cowman A.F., Kemp D.J.;
RT "Amplification of the multidrug resistance gene in some chloroquine-resistant isolates of *P. falciparum*.";
RL Cell 57:921-930(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92017800; PubMed=1922044;
RA Trigilia T., Foote S.J., Kemp D.J., Cowman A.F.;
RT "Amplification of the multidrug resistance gene pfmdr1 in Plasmodium falciparum has arisen as multiple independent events.";
RL Mol. Cell. Biol. 11:5244-5250(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149200; PubMed=8426608;
RA Wilson C.M., Volkman S.K., Thaitong S., Martin R.K., Kyle D.E., Milhous W.K., Wirth D.F.;
RT "Amplification of pfmdr1 associated with mefloquine and halofantrine resistance in Plasmodium falciparum from Thailand.";
RL Mol. Biochem. Parasitol. 57:151-160(1993).
CC -1- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: *P. FALCIPARUM* RESISTANT TO THE DRUG CHLOROQUINE HAVE MULTIPLE COPIES OF THE GENE CODING FOR MDR.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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CC EMBL; M29154; AAA29646.1; -;
DR EMBL; X56851; CAA40180.1; -;
DR EMBL; S53996; AAD13870.1; -;
DR PIR; A32547; DVZQF.
DR PIR; S18204; S18204.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtransportrTM.
DR Pfam; PF000005; ABC_tran; 2.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transportr; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 82 POTENTIAL.
FT TRANSMEM 91 116 POTENTIAL.
FT TRANSMEM 160 188 POTENTIAL.
FT TRANSMEM 194 212 POTENTIAL.
FT TRANSMEM 279 298 POTENTIAL.
FT TRANSMEM 314 338 POTENTIAL.
FT DOMAIN 339 788 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 789 807 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 908 928 POTENTIAL.
FT TRANSMEM 1028 1048 POTENTIAL.
FT TRANSMEM 1063 1083 POTENTIAL.
FT DOMAIN 1084 1419 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 643 661 POLY-ASN.

FT NP_BIND 413 420 ATP (POTENTIAL).
FT NP_BIND 1161 1168 ATP (POTENTIAL).
FT REPEAT 1 721
FT REPEAT 722 1419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1419 AA; 162251 MW; 0F96C7C1850B33D0 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 1419;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSLDS 7
| | | | | | | |
DB 1338 ATSSLDS 1344
RESULT 6
SON_MOUSE
ID SON_MOUSE STANDARD; PRT; 2404 AA.
AC O9QX47; O9QXP5; O9CQK6; O9CQ12;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE SON protein.
GN SON.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX STRAIN=129/SV;
RX MEDLINE=2040886; PubMed=10950926;
RA Wynn S.L., Fisher R.A., Pagel C., Price M., Liu Q.Y., Khan I.M., Zammit P., Dadgar K., Mazrani W., Kessling A., Lee J.S., Bulwela L.;
RT "Organization and conservation of the GART/SON/DONSON locus in mouse and human genomes.";
RL Genomics 68:57-62(2000).
RN [2]
RP SEQUENCE OF 1-116 FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Hippocampus, Small intestine, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: Transcriptional repressor. Binds to the consensus DNA sequence: 5'-GAGTAN[CG]AGCC-3'. Might protect cells from apoptosis. Might be involved in pre-mRNA splicing (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- DOMAIN: Contains 8 types of repeats which are distributed in 3 regions.

CC -!- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF193606; AAF23120.1; -
 DR EMBL; AF193595; AAF23120.1; JOINED.
 DR EMBL; AF193596; AAF23120.1; JOINED.
 DR EMBL; AF193597; AAF23120.1; JOINED.
 DR EMBL; AF193598; AAF23120.1; JOINED.
 DR EMBL; AF193599; AAF23120.1; JOINED.
 DR EMBL; AF193600; AAF23120.1; JOINED.
 DR EMBL; AF193601; AAF23120.1; JOINED.
 DR EMBL; AF193602; AAF23120.1; JOINED.
 DR EMBL; AF193603; AAF23120.1; JOINED.
 DR EMBL; AF193604; AAF23120.1; JOINED.
 DR EMBL; AF193605; AAF23120.1; JOINED.
 DR EMBL; AF193607; AAF23121.1; -
 DR EMBL; AK019312; BAB31659.1; -
 DR EMBL; AK019081; BAB31536.1; -
 DR EMBL; AK008478; BAB25691.1; -
 DR EMBL; AK008256; BAB25562.1; -
 DR MGD; MGI:98353; Son. -
 DR InterPro; IPR001159; DS_RBD.
 DR InterPro; IPR000467; G_patch.
 DR Pfam; PF00035; dsrm; 1.
 DR Pfam; PF01585; G_patch; 1.
 DR SMART; SM00443; G_patch; 1.
 DR PROSITE; PS0137; DS_RBD; 1.
 DR PROSITE; PS0174; G_PATCH; 1.
 KW RNA-binding; DNA-binding; Nuclear protein; Repeat;
 KW Alternative splicing.
 FT DOMAIN 721 850
 FT 13 X 10 AA TANDEM REPEATS OF L-A-[ST]-
 FT [NSG]-[TS]-MDSOM.
 FT 11 X 7 AA TANDEM REPEATS OF [DR]-P-Y-R-
 FT [LI][AG][QHP].
 FT 14 X 6 AA REPEATS OF [ED]-R-S-M-M-S.
 FT 1-1.
 FT 1-2.
 FT 1-3.
 FT 1-4.
 FT 1-5.
 FT 1-6.
 FT 1-7.
 FT 1-8.
 FT 1-9.
 FT 1-10.
 FT 1-11.
 FT 1-12.
 FT 1-13.
 FT 1-14.
 FT 3 X 11 AA TANDEM REPEATS OF P-P-L-P-P-E-E-
 FT P-P-[TME]-[MTG].
 FT 7 X 7 AA REPEATS OF P-S-R-R-S-R-[TS].
 FT 2-1.
 FT 2-2.
 FT 2-3.
 FT 2-4.
 FT 2-5.
 FT 2-6.
 FT 2-7 (APPROXIMATE).
 FT 2 X 19 AA REPEATS OF P-S-R-R-R-R-S-R-S-V-
 FT V-R-R-R-S-F-S-I-S.
 FT 3-1.
 FT 3-2 (APPROXIMATE).
 FT 3 X TANDEM REPEATS OF [ST]-P-[VLII]-R-
 FT [RL]-[RK]-[RF]-S-R.

FT DOMAIN 2283 2329 G-PATCH.
 FT VARSPLIC 2349 2404 DRBM.
 FT VARSPLIC 2086 2086 K -> F (IN ISOFORM 2).
 FT VARSPLIC 2087 2404 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 2404 AA; 261428 MW; 648BF28ED3FC01D9 CRC64;
 Query Match 93.5%; Score 29; DB 1; Length 2404;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSSIDS 7
 DB 802 ATSSMDS 808
 RESULT 7
 SON_HUMAN STANDARD; PRT: 2426 AA.
 ID SON_HUMAN Q9UPY0; Q14120; Q14487; Q9UKP9; Q9H7B1; Q9P070;
 AC Q9P072;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SON protein (SON3) (Negative regulatory element-binding protein) (NRE-
 DE binding protein) (DBP-5) (Box antagonist selected in saccharomyces 1)
 DE (BASS1) (Protein C21orf50).
 OS SON OR NREBP OR DBP5 OR C21ORF50 OR KIAA1019.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D; E AND F).
 RX MEDLINE=21564202; PubMed=11707072;
 RA Raymond A., Friedli M., Neergaard Henriksen C., Chapot F.,
 RA Deutsch S., Ucla C., Rossier C., Lyle R., Guipponi M.,
 RA Antonarakis S.E.;
 RT "From PREDs and open reading frames to cDNA isolation: revisiting the
 RT human chromosome 21 transcription map.";
 RL Genomics 78:46-54(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM G).
 RC TISSUE=Liver;
 RX MEDLINE=21316479; PubMed=11306577;
 RA Sun C.-T., Lo W.-Y., Wang I.-H., Lo Y.-H., Shiou S.-R., Lai C.-K.,
 RA Ting L.-P.;
 RT "Transcription repression of human hepatitis B virus genes by negative
 RT regulatory element-binding protein/SON";
 RL J. Biol. Chem. 276:24059-24067(2001).
 RN [3]
 RP SEQUENCE OF 1-689 FROM N.A. (ISOFORM H).
 RC TISSUE=Placenta;
 RA Casadei R., Strippoli P., D'Addabbo P., Canaider S., Lenzi L.,
 RA Vitale L., Giannone S., Carinci P., Zannotti M.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-130 FROM N.A.
 RC TISSUE=Smooth muscle;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-114 FROM N.A.
 RC TISSUE=Blood;
 RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
 RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
 RT "Human partial CDS from cd34+ stem cells";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP SEQUENCE OF 437-2426 FROM N.A. (ISOFORM B).
RC TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
RN [7]
RN SEQUENCE OF 554-2426 FROM N.A. (ISOFORM A).
RX MEDLINE=92049296; PubMed=1944255;
RA Chumakov I.M., Berdichevskii F.B., Sokolova N.V., Reznikov M.V.,
RA Prasolov V.S.;
RA "Identification of a protein product of a novel human gene SON and
RT the biological effect upon administering a changed form of this gene
RT into mammalian cells.";
RL Mol. Biol. (Mosk) 25:731-740(1991).
RN [8]
RN SEQUENCE OF 709-1079 FROM N.A. (ISOFORM I).
RC TISSUE=Placenta;
RX MEDLINE=93062885; PubMed=1435774;
RA Bliskovskii V.V., Kirillov A.V., Zakhariev V.M., Chumakov I.M.;
RA "The human son gene: the large and small transcripts contains various
RT 5'-terminal sequences.";
RL Mol. Biol. (Mosk) 26:807-812(1992).
RN [9]
RN SEQUENCE OF 1009-1131 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93062884; PubMed=1435773;
RA Bliskovskii V.V., Berdichevskii F.B., Tkachenko A.V., Belova M.E.,
RA Chumakov I.M.;
RA "Coding part of the son gene small transcript contains four areas of
RT complete tandem repeats.";
RL Mol. Biol. (Mosk) 26:793-806(1992).
RN [10]
RN SEQUENCE OF 1145-2426 FROM N.A. (ISOFORM F).
RX MEDLINE=93048367; PubMed=1424986;
RA Mattioli T., Hume C.R., Konigorski S., Hayes P., Osterweil Z.,
RA Lee J.S.;
RA "A cDNA clone for a novel nuclear protein with DNA binding
RT activity.";
RL Chromosoma 101:618-624(1992).
RN [11]
RN SEQUENCE OF 1692-2175 FROM N.A. (ISOFORM A).
RX MEDLINE=89039788; PubMed=3054499;
RA Berdichevskii F.B., Chumakov I.M., Kiselev L.L.;
RA "Decoding of the primary structure of the son3 region in human
RT genome: identification of a new protein with unusual structure and
RT homology with DNA-binding proteins.";
RL Mol. Biol. (Mosk) 22:794-801(1988).
RN [12]
RN SEQUENCE OF 1939-2426 FROM N.A. (ISOFORM J).
RC TISSUE=Cerebellum;
RX MEDLINE=99439804; PubMed=10509013;
RA Greenhalf W., Lee J., Chaudhuri B.;
RA "A selection system for human apoptosis inhibitors using yeast.";
RT Yeast 15:1307-1321(1999).
CC -1- FUNCTION: Represses hepatitis B virus (HBV) core promoter activity
CC and transcription of HBV genes and production of HBV virions.
CC Binds to the consensus DNA sequence: 5'-GA[GT]AN[CG][AG]CC-3'.
CC Might protect cells from apoptosis. Might be involved in pre-mRNA
CC splicing (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear with a speckled distribution.
CC -1- ALTERNATIVE PRODUCTS: 10 isoforms; A, B, C, D, E, F (shown here),
CC G, H, I and J; may be produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Widely expressed, with the higher expression
CC seen in leukocyte and heart.
CC -1- DOMAIN: Contains 8 types of repeats which are distributed in 3
CC regions.
CC -1- SIMILARITY: Colocalizes with the pre-mRNA splicing factor
CC SFRS2/SC-35.
CC -1- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
CC -1- CAUTION: ISOFORM A SEQUENCE FROM REF.7 DIFFERS FROM THAT SHOWN
CC DUE TO A FRAMESHIFT.
CC -1- CAUTION: ISOFORM F SEQUENCE FROM REF.10 DIFFERS FROM THAT SHOWN
CC DUE TO A FRAMESHIFT.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF380179; AAL34497.1; -
DR EMBL; X63753; CAA45282.1; ALT_FRAME.
DR EMBL; M36428; AAA36624.1; -
DR EMBL; AF380180; AAL34498.1; -
DR EMBL; AF380181; AAL34499.1; -
DR EMBL; AF380182; AAL34500.1; -
DR EMBL; AF380183; AAL34501.1; -
DR EMBL; AF380184; AAL34502.1; -
DR EMBL; AY026895; AAK07692.1; -
DR EMBL; AF435977; AAL30810.1; -
DR EMBL; X63751; CAC69885.1; -
DR EMBL; AB028942; BAA82971.1; -
DR EMBL; X63071; CAA44793.1; ALT_FRAME.
DR EMBL; AF139897; AAB23945.1; -
DR EMBL; AK024752; BAB14985.1; -
DR EMBL; AF161428; AAF28988.1; -
DR EMBL; AF161430; AAF28990.1; -
DR PIR; PNO099; PNO099.
DR Genew; HGNC:11183; SON.
DR MIM; 182465; -
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR000467; G_patch.
DR Pfam; PF00355; dsrm; 1.
DR Pfam; PF01585; G_patch; 1.
DR SMART; SM00443; G_patch; 1.
DR PROSITE; PS50137; DS_RBD; 1.
DR PROSITE; PS50174; G_PATCH; 1.
KW RNA-binding; DNA-binding; Nuclear protein; Repeat;
KW Alternative splicing.
TABLE
DOMAIN 726 895
DOMAIN 912 988
DOMAIN 1006 1126
REPEAT 1006 1011
REPEAT 1014 1019
REPEAT 1021 1026
REPEAT 1030 1035
REPEAT 1038 1043
REPEAT 1046 1051
REPEAT 1055 1060
REPEAT 1063 1068
REPEAT 1071 1076
REPEAT 1080 1085
REPEAT 1089 1094
REPEAT 1100 1105
REPEAT 1111 1116
REPEAT 1121 1126
REPEAT 1147 1179
DOMAIN 1359 1390
DOMAIN 1925 1994
REPEAT 1925 1931
REPEAT 1953 1959
REPEAT 1960 1966
Query Match 93.5%; Score 29; DB 1; Length 2426;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
||||:|

Db 827 ATSSMDS 833

RESULT 8

LMRA_LACLA STANDARD; PRT; 584 AA.
AC Q9CHL8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding and permease protein.
GN LMRA OR LL0711.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Winkler P., Mager S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis ILL403";
RL Genome Res. 11:731-733(2001).
CC -|- FUNCTION: Efflux transporter for a variety of amphiphilic cationic
CC compounds, including antibiotics (By similarity).
CC -|- SUBUNIT: Homodimer (Potential).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -|- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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CC -----
CC EMBL; A5006305; AAK04809.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001140; ABC_transporter_TM.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF00664; ABC_membrane; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
KW ATP-binding; Transport; Transmembrane; Antibiotic resistance;
KW Complete proteome.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 144 164 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
FT TRANSMEM 255 275 POTENTIAL.
FT TRANSMEM 286 306 POTENTIAL.
FT NP_BIND 376 383 ATP (POTENTIAL).
SQ SEQUENCE 584 AA; 63999 MW; 89F13E5926410462 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 584;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
||||:|

Db 507 ATASLDS 513

RESULT 9

LMRA_LACLC STANDARD; PRT; 584 AA.
AC P97046;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Multidrug resistance ABC transporter ATP-binding and permease protein.
GN LMRA.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG1363;
RX MEDLINE=97008061; PubMed=8855237;
RA van Veen H.W., Venema K., Bolhuis H., Oussenko I., Kok J., Poolman B.,
RA Driessen A.J., Konings W.N.;
RT "Multidrug resistance mediated by a bacterial homolog of the human
multidrug transporter MDR1";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10668-10672(1996).
CC -|- FUNCTION: Efflux transporter for a variety of amphiphilic cationic
CC compounds, including antibiotics.
CC -|- SUBUNIT: Homodimer (Potential).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -|- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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CC -----
CC EMBL; U63741; AAB49750.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001140; ABC_transporter_TM.
DR Pfam: PF00005; ABC_tran; 2.
DR Pfam: PF00664; ABC_membrane; 2.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 2.
KW ATP-binding; Transport; Transmembrane; Antibiotic resistance.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 144 164 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
FT TRANSMEM 255 275 POTENTIAL.
FT TRANSMEM 286 306 POTENTIAL.
FT NP_BIND 376 383 ATP (POTENTIAL).
SQ SEQUENCE 584 AA; 63918 MW; C8E1CD9469C3A725 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 584;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

||||:|

Db 507 ATASLDS 513

RESULT 10

Y4GM_RHISN STANDARD; PRT; 586 AA.
ID Y4GM_RHISN
AC P55469;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ABC transporter ATP-binding protein Y4GM.
GN Y4GM.

```

OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_taxid=394;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
CC -----
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CC -----
DR EMBL; AE000075; AAB91687.1; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001140; ABCtransportrTM.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR Hypothetical protein; ATP-binding; Transport; Transmembrane; Plasmid.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 66 86 POTENTIAL.
FT TRANSMEM 152 172 POTENTIAL.
FT TRANSMEM 256 276 POTENTIAL.
FT NP_BIND 379 386 ATP (POTENTIAL).
SQ SEQUENCE 586 AA; 64262 MW; 1095DFEB82620637 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 586;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 509 ATSALDS 515

RESULT 11
HEPA_ANASP STANDARD; PRT; 607 AA.
AC P22638;
DT 01-AUG-1991 (Rel. 19, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heterocyst differentiation ATP-binding protein hepA.
GN HEPA OR HETA OR ALR2835.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_taxid=103690;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90264305; PubMed=2111805;
RA Holland D., Wolk C.P.;
RT "Identification and characterization of hetA, a gene that acts early
RT in the process of morphological differentiation of heterocysts.";
RL J. Bacteriol. 172:3131-3137(1990).
RN [2]
RN REVISIONS.
RP Zhu J., Wolk C.P.;
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.

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RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -!- FUNCTION: ACTS EARLY IN THE PROCESS OF MORPHOLOGICAL
CC DIFFERENTIATION OF HETEROCYSTIS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- INDUCTION: BY DEPRIVATION OF NITRATE.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF031959; AAC32400.1; ALT_INIT.
DR EMBL; AP003591; BAB74534.1; -
DR PIR; A35391; A35391.
DR HSP; P13569; INBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001140; ABCtransportrTM.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR Heterocyst; ATP-binding; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 88 110 POTENTIAL.
FT TRANSMEM 163 182 POTENTIAL.
FT TRANSMEM 186 208 POTENTIAL.
FT TRANSMEM 285 307 POTENTIAL.
FT NP_BIND 397 404 ATP (POTENTIAL).
SQ SEQUENCE 607 AA; 67789 MW; B47970D4758F564F CRC64;

Query Match 90.3%; Score 28; DB 1; Length 607;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 527 ATSALDS 533

RESULT 12
YAS1_HAEIN STANDARD; PRT; 614 AA.
AC Q57180; O05043;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein HI1051.
GN HI1051.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus
OX NCBI_taxid=727;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Rd / Kw20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

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RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD."
RL Science 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
CC
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CC
CC EMBL: U32785; AAC22709.1; -.
DR TIGR: H11051; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001140; ABCtranprtTM.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF00664; ABC_membrane; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW Hypothetical protein; ATP-binding; Transport; Transmembrane;
KW Complete proteome.
FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 157 177 POTENTIAL.
FT TRANSMEM 178 198 POTENTIAL.
FT NP_BIND 397 404 ATP (POTENTIAL).
SQ SEQUENCE 614 AA; 68398 MW; 306BBA9646921EA0 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 614;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 532 ATSLDS 538
|||||

RESULT 13
MDL1_CANAL
ID MDL1_CANAL STANDARD; PRT; 685 AA.
AC P97998;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP-dependent permease MDL1.
GN MDL1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=491A;
RA McCreath K.J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC
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CC
CC EMBL: Y12327; CAA72996.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001140; ABCtranprtTM.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF00664; ABC_membrane; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transmembrane; Glycoprotein; Transport.
FT TRANSMEM 96 116 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 256 276 POTENTIAL.
FT TRANSMEM 354 374 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT NP_BIND 475 482 ATP (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 576 576 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 685 AA; 75868 MW; 46239E214CE1267A CRC64;

Query Match 90.3%; Score 28; DB 1; Length 685;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7
DB 606 ATSLDS 612
|||||

RESULT 14
MDL1_YEAST
ID MDL1_YEAST STANDARD; PRT; 695 AA.
AC P33310;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-dependent permease MDL1.
GN MDL1 OR YLR188W OR I9470.3.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94287714; PubMed=7912468;
RA Dean M.C., Allikmets R., Gerrard B.C., Stewart C., Kistler A.,
RA Shfer B., Michaelis S., Strathern J.;
RT "Mapping and sequencing of two yeast genes belonging to the
RT ATP-binding cassette superfamily.";
RL Yeast 10:377-383(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kottler P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharte M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
```

RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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CC -----
DR EMBL; U17246; AAB67455.1; -;
DR EMBL; L16958; AAA20681.1; -;
DR PIR; S42681; S42681.
DR SGD; S0004178; MDL1.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001140; ABCtransportTM.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Transmembrane; Glycoprotein; Transport.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT TRANSMEM 338 358 POTENTIAL.
FT TRANSMEM 372 392 POTENTIAL.
FT NP_BIND 467 474 ATP (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 22 22 A -> G (IN REF. 1).
FT CONFLICT 150 150 F -> L (IN REF. 1).
FT CONFLICT 267 268 GA -> WP (IN REF. 1).
FT CONFLICT 313 314 NE -> KQ (IN REF. 1).
FT CONFLICT 417 432 RPTIGKDPVSLAQKPI -> SSDYWKGVSPKTHR
FT (IN REF. 1).
SQ SEQUENCE 695 AA; 75950 MW; 3175B17FBD779BBE CRC64;
Query Match 90.3%; Score 28; DB 1; Length 695;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
Db 600 ATSALDS 606
III:III

RESULT 15
CVAB_ECOLI STANDARD; PRT; 698 AA.
AC P22520;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Colicin V secretion ATP-binding protein cvab.
GN CVAB.
OS Escherichia coli.
OG Plasmid IncFI ColV3-K30.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE-91065315; PubMed-2249654;
RA Gilson L., Mahanty H.K., Kolter R.;
RT "Genetic analysis of an MDR-like export system: the secretion of
RT colicin V.";
RL EMBO J. 9:3875-3884(1990).
RN [2]
RP SEQUENCE OF 373-698 FROM N.A.
RX MEDLINE-98416173; PubMed-9743528;
RA Otto B.R., van Dooren S.J.M., Nuijens J.H., Luijckx J., Oudega B.;
RT Characterization of a hemoglobin protease secreted by the pathogenic
RT Escherichia coli strain EBL-;
RL J. Exp. Med. 188:1091-1103(1998).
CC -1- FUNCTION: INVOLVED, IN CONJUNCTION WITH CVAA, IN THE SECRETION OF
CC COLICIN V.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. HLYB SUBFAMILY.
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CC -----
DR EMBL; X57524; CAA40744.1; -;
DR EMBL; AJ223631; CAA11515.1; -;
DR PIR; S1272; IREC5B.
DR MEROPS; C39 UPW; -;
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001140; ABCtransportTM.
DR InterPro; IPR005074; Peptidase_C39.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF03412; Peptidase_C39; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR Plasmid; Transport; Protein transport; Bacteriocin transporter;
KW Transmembrane; ATP-binding.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 211 231 POTENTIAL.
FT TRANSMEM 289 311 POTENTIAL.
FT TRANSMEM 315 334 POTENTIAL.
FT TRANSMEM 412 432 POTENTIAL.
FT NP_BIND 526 533 ATP (BY SIMILARITY).
SQ SEQUENCE 698 AA; 78245 MW; 47FC40510AF5D28A CRC64;
Query Match 90.3%; Score 28; DB 1; Length 698;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSIDS 7
Db 656 ATSALDS 662
III:III

Search completed: March 10, 2003, 16:57:46
Job time : 6.34483 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 5.58621 seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	42	89.4	130	1 KV5G_MOUSE	P01639 mus musculus
2	37	78.7	128	1 KV3K_HUMAN	P08311 homo sapien
3	36	76.6	282	1 PSTA_HAEIN	P45190 haemophilus
4	36	76.6	947	1 PM19_CHLPN	Q92813 chlamydia p
5	35	74.5	108	1 KV3A_HUMAN	P01619 homo sapien
6	35	74.5	117	1 KV5H_MOUSE	P01641 mus musculus
7	35	74.5	1897	1 PTPF_HUMAN	P10586 homo sapien
8	34	72.3	129	1 KV3M_HUMAN	P18136 homo sapien
9	34	72.3	131	1 Y15K_MDV	P06848 wheat dwarf
10	34	72.3	250	1 QCRB_BACST	Q45659 bacillus st
11	34	72.3	287	1 PSTA_XYLF	Q99bk1 xylella fas
12	34	72.3	461	1 DCUC_ECOLI	Q47134 escherichia
13	33	70.2	108	1 KV1R_HUMAN	P01610 homo sapien
14	33	70.2	351	1 RNFD_YERPE	Q82ed2 yersinia pe
15	32	68.1	108	1 KV1O_HUMAN	P01607 homo sapien
16	32	68.1	128	1 YG35_CYAPA	P48275 cyanophora
17	32	68.1	527	1 VG12_BPT4	P10930 bacterioph
18	32	68.1	552	1 MGRA_METJA	Q60391 methanococc
19	32	68.1	658	1 LITB_STRPN	Q924p7 streptococc
20	32	68.1	854	1 SBP2_HUMAN	Q96t21 homo sapien
21	32	68.1	2244	1 PYR1_SCHPO	Q09794 schizosacch
22	31	66.0	85	1 Y12K_MSVS	P14993 maize stre
23	31	66.0	108	1 KV1V_HUMAN	P04430 homo sapien
24	31	66.0	109	1 KV3B_HUMAN	P01620 homo sapien
25	31	66.0	352	1 RNFD_ECO57	P58325 escherichia
26	31	66.0	352	1 RNFD_ECOLI	P76182 escherichia
27	31	66.0	352	1 RNFD_SALTI	Q826q8 salmonella
28	31	66.0	352	1 RNFD_SALTY	Q82pm3 salmonella
29	31	66.0	470	1 VL2_HPV54	Q81023 human papil
30	31	66.0	497	1 SPK1_DUGTI	P42687 dugesia lig
31	31	66.0	511	1 EGR1_BRARE	P28632 brachydanio
32	31	66.0	556	1 C4G1_DROME	Q9V3s0 drosophila
33	31	66.0	565	1 HXB1_HAEIN	P44601 haemophilus

RESULT 1
KV5G_MOUSE
ID KV5G_MOUSE STANDARD; PRT; 130 AA.
AC P01639; P01640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 41 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79221900; PubMed=111146;
RA Seidman J.G., Max E.E., Leder P.;
RT "A kappa-immunoglobulin gene is formed by site-specific recombination
RT without further somatic mutation";
RL Nature 280:370-375(1979).
RN [2]
RP SEQUENCE OF 1-33.
RX MEDLINE=77148916; PubMed=403522;
RA Burstein Y., Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
RT precursors of mouse immunoglobulin lambdaI-type and kappa-type light
RT chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN [3]
RP SEQUENCE OF 23-130.
RX MEDLINE=67056897; PubMed=4162931;
RA Gray W.R., Dreyer W.J., Hood L.;
RT "Mechanism of antibody synthesis: size differences between mouse
RT kappa chains.";
RL Science 155:465-467(1967).
CC -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
CC SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01922; KVM5M4.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_LV.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal; Bence-Jones protein.
FT SIGNAL 1 22
FT CHAIN 23 130
FT DOMAIN 23 45
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT VARIANT 1 2
FT NON_TER 130 130

P45356 haemophilus
P23468 homo sapien
P01622 homo sapien
P01625 homo sapien
Q92kx2 helicobacte
P56133 helicobacte
P56402 mus musculu
P34080 rattus norv
O51927 buchnera ap
Q8udn3 agrobacteri
P42032 rhodobacter
Q97rel streptococc

ALIGNMENTS

Probable outer membrane protein pmp19 precursor (Polymorphic membrane protein 19).
 PMP19 OR CPN0539 OR CP0213.
 Chlamydia pneumoniae (Chlamydia pneumoniae).
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia. NCBI_TaxID=83558;

[1]
 NCBI_TaxID=83558;
 SEQUENCE FROM N.A.
 STRAIN=CWL029;
 MEDLINE=99206606; PubMed=10192388;
 Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=AR39;
 MEDLINE=20150255; PubMed=10684935;
 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
 "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
 [3]
 SEQUENCE FROM N.A.
 STRAIN=J138;
 MEDLINE=20330349; PubMed=10871362;
 Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
 [4]
 SEQUENCE FROM N.A.
 STRAIN=J138;
 MEDLINE=20299986; PubMed=10839753;
 Shirai M., Hirakawa H., Ouchi K., Tabuchi M., Kishi F., Kimoto M., Takeuchi H., Nishida J., Shibata K., Fujinaga R., Yoneda H., Matsushina H., Tanaka C., Furukawa S., Miura K., Nakazawa A., Ishii K., Shiba T., Hattori M., Kuhara S., Nakazawa T.;
 "Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States."; J. Infect. Dis. 181 Suppl 3:S524-S527(2000).
 -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).
 -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.

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EMBL; AE001638; AAD18679.1; -
 EMBL; AE002181; AAF38083.1; -
 EMBL; AP002547; BAA98745.1; -
 HSSP; Q90121; 1KPT.
 TIGR; CP0213; -
 InterPro; IPR003368; Chlamydia_PMP.
 InterPro; IPR003357; OMP.
 Pfam; PF02385; OMP; 1.
 Pfam; PF02415; DUF145; 1.
 Outer membrane; Signal; Multigene family; Complete proteome.
 SIGNAL 1 19 POTENTIAL
 CHAIN 20 947 PROBABLE OUTER MEMBRANE PROTEIN PMP19.
 CONFLICT 453 453 E -> D (IN REF. 3).
 SEQUENCE 947 AA; 103642 MW; 20CE1DEEE1606DFF CRC64;

Query Match 76.6%; Score 36; DB 1; Length 947;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYASSPYT 9
 :||| |||
 Db 560 EYASKPYT 567

RESULT 5

ID KV3A_HUMAN STANDARD; PRT; 108 AA.
 AC P01619;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region B6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA Milstein C.;
 RT "The basic sequences of immunoglobulin kappa chains: sequence studies of Bence Jones proteins Rad, Fr4 and B6."; FEBS Lett. 2:301-304(1969).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01891; K3HUB6.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IG; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89
 FT NON_TER 108 108
 FT BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 74.5%; Score 35; DB 1; Length 108;
 Best Local Similarity 75.0%; Pred. No. 3;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYASSPYT 9
 :||| |||
 Db 91 QYSSPFT 98

RESULT 6

ID KV5H_MOUSE STANDARD; PRT; 117 AA.
 AC P01641;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region MOPC 173B precursor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81064681; PubMed=6777049;
 RA Max E.E., Seidman J.G., Miller H., Leder P.;
 RT "Variation in the crossover point of kappa immunoglobulin gene V-J recombination: evidence from a cryptic gene."; Cell 21:793-799(1980).
 RL Cell 21:793-799(1980).
 CC -----

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: K00880; AAA39031.1; -
 DR PIR: A01924; KWSB3B.
 DR HSSP: P01607; IREI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin v region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 117 IG KAPPA CHAIN V-V REGION MOPC 173B.
 FT DOMAIN 23 45 FRAMEWORK-1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 57 71 FRAMEWORK-2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 79 110 FRAMEWORK-3.
 FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12954 MW; 24B3D4B9AC2E4D6C CRC64;

Query Match 74.5%; Score 35; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOYASSP 7
 |||||
 DB 111 LOYASSP 117

RESULT 7

PTPE_HUMAN STANDARD; PRT; 1897 AA.
 AC P10586;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE LAR protein precursor (Leukocyte antigen related) (BC 3.1.3.4B).
 GN PTPRF OR LAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Tonsil;
 RX MEDLINE=89035978; PubMed=2972792;
 RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;
 RT "A new member of the immunoglobulin superfamily that has a
 RT cytoplasmic region homologous to the leukocyte common antigen.";
 RL J. Exp. Med. 168:1523-1530(1988).
 RN [2]
 RP MUTAGENESIS.
 RX MEDLINE=90046860; PubMed=2554325;
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
 RT "A family of receptor-linked protein tyrosine phosphatases in humans
 RT and Drosophila.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
 RN [3]
 RP MUTAGENESIS.
 RX MEDLINE=90316093; PubMed=1695146;
 RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
 RT "Distinct functional roles of the two intracellular phosphatase like
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and
 RT LAR.";
 RL EMBO J. 9:2399-2407(1990).
 CC -1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.
 CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
 CC (PTPASE).
 CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE

CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC FIRST ONE.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O -> protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: Y00815; CAA68754.1; -
 DR PIR: S03841; TDHULK.
 DR HSSP: P18052; IYFO.
 DR Genew: HGNC:9670; PTPRF.
 DR MIM: 179590;
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003962; FNIII_repeat.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 7.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART: SM00060; FN3; 5.
 DR SMART: SM00408; IGC2; 3.
 DR SMART: SM00194; PTEC; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
 KW Cell adhesion; Immunoglobulin domain; Repeat.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 1897 LAR PROTEIN.
 FT DOMAIN 17 1250 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1251 1274 POTENTIAL.
 FT DOMAIN 1275 1897 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1360 1606 PROTEIN-TYROSINE PHOSPHATASE 1.
 FT DOMAIN 1649 1897 PROTEIN-TYROSINE PHOSPHATASE 2.
 FT ACT_SITE 1538 1538 BY SIMILARITY.
 FT ACT_SITE 1829 1829 BY SIMILARITY.
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 711 711 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 956 956 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 1538 1538 C->S: LOSS OF ACTIVITY.
 SQ SEQUENCE 1897 AA; 211844 MW; 439850F1D5C031FF CRC64;

Query Match 74.5%; Score 35; DB 1; Length 1897;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
 :|||||
 DB 1226 QYASSPYS 1233

RESULT 8

KV3M_HUMAN STANDARD; PRT; 129 AA.
 ID KV3M_HUMAN
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; PLO021; K3HUHL.
DR HSSP; P80362; IWTLL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 72.3%; Score 34; DB 1; Length 129;
Best Local Similarity 75.0%; Pred. No. 5.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
DB 111 QYGSSPWT 118

RESULT 9
Y15K_WDV
ID Y15K_WDV STANDARD; PRT; 131 AA.
AC P06848;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Hypothetical 15 kDa protein.
OS Wheat dwarf virus (WDV).
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OX NCBI_TaxID=10834;
RN [1]
RP SEQUENCE FROM N.A.
RA McDowell S.W., McDonald H., Hamilton W.D.O., Coutts R.H.A.,
RA Buck K.W.;
RT "The nucleotide sequence of cloned wheat dwarf virus DNA.";
RL EMBO J. 4:2173-2180(1985).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X02869; CAA26623.1; -.

DR PIR; C24356; C24356.
KW Hypothetical protein.
SQ SEQUENCE 131 AA; 14687 MW; CE890568A150FCF3 CRC64;

Query Match 72.3%; Score 34; DB 1; Length 131;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YASSPYT 9
DB 101 FASSPYT 107

RESULT 10
QCRC_BACST
ID QCRC_BACST STANDARD; PRT; 250 AA.
AC Q45659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Menquinol-cytochrome C reductase cytochrome B/C subunit.
GN QCRC
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacilliales; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1041;
RX MEDLINE=96218169; PubMed=8647852;
RA Sone N., Tsuchiya N., Inoue M., Noguchi S.;
RT "Bacillus stearothermophilus qcr operon encoding rieske Fes protein,
RT cytochrome b6, and a novel-type cytochrome c1 of quinol-cytochrome c
RT reductase.";
RL J. Biol. Chem. 271:12457-12462(1996).
CC -I- FUNCTION: COMPONENT OF THE MENAQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX.
CC -I- SUBUNIT: THE MAIN SUBUNITS OF THE MENAQUINONE-CYTOCHROME C COMPLEX
CC ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A CYTOCHROME B/C
CC SUBUNIT.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESPONDS TO THE
CC CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.
CC -----
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CC -----
DR EMBL; D83789; BAA12118.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; Cyt_C1.
DR InterPro; IPR000179; Cyt_b6.
DR Pfam; PF00034; cytochrome_c; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00193; CYTOCHROME_B_OO; 1.
KW Electron transport; Transmembrane; Heme.
FT TRANSMEM 46 62 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT BINDING 192 192 HEME (COVALENT) (POTENTIAL).
FT BINDING 195 195 HEME (COVALENT) (POTENTIAL).
FT METAL 196 196 IRON (HEME AXIAL LIGAND) (POTENTIAL).
SQ SEQUENCE 250 AA; 27342 MW; E6D57CF486430306 CRC64;

Query Match 72.3%; Score 34; DB 1; Length 250;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YASSPYT 9
DB 111 III

Db 97 YASGPVT 103

RESULT 11

PSTA_XYLFA

ID PSTA_XYLFA STANDARD; PRT; 287 AA.

AC Q9PBK1; 109 131

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Phosphate transport system permease protein pstA.

GN PSTA OR XF2143.

OS Xylella fastidiosa.

OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

OC Xylella.

OX NCBI_TaxID=2371;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=9a5c;

RX MEDLINE=20365717; PubMed=10910347;

RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,

RA Bueno M.R.P., Camargo A.A., Canargo L.E.A., Carraro D.M., Carrer H.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,

RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

RA Menck C.F.M., Miracca E.C., Miyaki C.V., Monteiro-Vitorello C.B.,

RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,

RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,

RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsunako M.H.,

RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;

RT "The genome sequence of the plant pathogen Xylella fastidiosa.";

RL Nature 406:151-159(2000).

CC -!- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

CC FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE

CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

CC (By similarity).

CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT

CC SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.

CC -----

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CC -----

CC EMBL; AE004029; AAF84942.1; -

CC InterPro: IPR000515; BPD.transp.

CC Pfam: PF00528; BPD.transp; 1.

CC TIGRFAMs: TIGR00974; 3a0107502c; 1.

CC PROSITE: PS00402; BPD_TRANSF_INN_MEMBR; 1.

CC Transport; Phosphate transport; Transmembrane; Inner membrane;

KW Complete proteome.

FT TRANSMEM 20 42 POTENTIAL.

FT TRANSMEM 75 97 POTENTIAL.

FT

FT TRANSMEM 109 131 POTENTIAL.
 FT TRANSMEM 136 158 POTENTIAL.
 FT TRANSMEM 190 212 POTENTIAL.
 FT TRANSMEM 252 274 POTENTIAL.
 SQ SEQUENCE 287 AA; 31060 MW; 1514AA618630505A CRC64;

Query Match

Best Local Similarity 72.3%; Score 34; DB 1; Length 287;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPY 8

Db 244 QFASSPY 250

DCUC_ECOLI STANDARD; PRT; 461 AA.

AC Q47134; Q92BC9; Q92BD0;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Anaerobic C4-dicarboxylate transporter dcuC.

GN DCUC OR B0621 OR Z0766 OR ECS0660.

OS Escherichia coli, and

OC Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562, 83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / AN387;

RX MEDLINE=97113548; PubMed=8955408;

RA Zientz E., Six S., Unden G.;

RT "Identification of a third secondary carrier (DcuC) for anaerobic

RT C4-dicarboxylate transport in Escherichia coli: roles of the three

RT Dcu carriers in uptake and exchange.";

RL J. Bacteriol. 178:7241-7247(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / W3110;

RX MEDLINE=97061202; PubMed=8905232;

RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,

RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

RA Mori H., Motomura K., Nakamura Y., Nishio Y., Saito N.,

RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

RA Yano M., Horiuchi T.;

RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 12.7-28.0 min region on the linkage map.";

RL DNA Res. 3:137-155(1996).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;

RX MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA

RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.:
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7";
RL Nature 409:529-533(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.:
RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / AN387;
RX MEDLINE=99296581; PubMed=10368146;
RA Zientz E., Janausch I.G., Six S., Unden G.:
RT "Functioning of DcuC as the C4-dicarboxylate carrier during glucose
RT fermentation by *Escherichia coli*.";
RL J. Bacteriol. 181:3716-3720(1999).
CC -1- FUNCTION: RESPONSIBLE FOR THE TRANSPORT OF C4-DICARBOXYLATES
CC DURING ANAEROBIC GROWTH.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE DCUC / DCUD (TC 2.A.61) FAMILY OF
CC TRANSPORTERS.
CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO THE
CC PRESENCE OF AN IS5 INSERTION ELEMENT BETWEEN CODONS 327 AND 328.
CC STRAIN W3110A BUT NOT W3110B HARBORS THIS IS5 INSERTION.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X99112; CAA67561.1; -
CC EMBL; AE000167; AAC73722.1; -
CC EMBL; U82598; AAB40821.1; -
CC EMBL; D90703; BAA35264.1; ALT_TERM.
CC EMBL; D90703; BAA35263.1; ALT_TERM.
CC EMBL; D90702; BAA35257.1; ALT_INIT.
CC EMBL; AE005241; AAG54956.1; -
CC EMBL; AP002552; BAB34083.1; -
CC EcoGene; EG13545; DcuC.
CC InterPro: IPR004669; DcuC.
CC Pfam; PF03606; DcuC; 1.
CC TIGRFAMs; TIGR00771; DcuC; 1.
KW Transmembrane; Inner membrane; Transport; Complete proteome.
FT TRANSMEM 2 22 POTENTIAL.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 267 287 POTENTIAL.
FT TRANSMEM 313 333 POTENTIAL.
FT TRANSMEM 343 363 POTENTIAL.
FT TRANSMEM 436 456 POTENTIAL.
SQ SEQUENCE 461 AA; 48412 MW; D4042FBFE9F5E2ED CRC64;

Query Match 72.38; Score 34; DB 1; Length 461;
Best Local Similarity 75.08; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOYASSPY 8
Db 110 LOYINSPI 117
RESULT 13
KVLR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.:
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC PIR; A01876; KIHUWE.
DR HSSP; P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
Query Match 70.28; Score 33; DB 1; Length 108;
Best Local Similarity 66.78; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LOYASSPY 9
Db 89 LOYSSFPWT 97
RESULT 14
RNFD_YERPE STANDARD; PRT; 351 AA.
AC Q8ZED2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electron transport complex protein rnfd.
GN RNFD OR YPO2242.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RL "Genome sequence of Yersinia pestis, the causative agent of plague."
CC Nature 413:523-527(2001).
CC
CC -!- FUNCTION: May be part of a membrane complex involved in electron
CC transport (By similarity).
CC
CC -!- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC,
CC rnfD, rnfE and rnfG (By similarity).
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC
CC -!- SIMILARITY: BELONGS TO THE NORB/RNFD FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; AJ414151; CAC91048.1; -
CC InterPro; IPR004338; NQR2_Rnfd_Rnfe.
CC Pfam; PF03116; NQR2_Rnfd_Rnfe; 1.
CC Electron transport; Transmembrane; Inner membrane; Complete proteome.
CC
CC TRANSMEM 21 43 POTENTIAL.
CC TRANSMEM 93 115 POTENTIAL.
CC TRANSMEM 122 144 POTENTIAL.
CC TRANSMEM 210 232 POTENTIAL.
CC TRANSMEM 237 259 POTENTIAL.
CC TRANSMEM 269 291 POTENTIAL.
CC TRANSMEM 298 315 POTENTIAL.
CC
CC SEQUENCE 351 AA; 38112 MW; A35EAE7524F605F8 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 351;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db :| |||||
1 MQIASSPFT 9

RESULT 15
KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;

RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01873; KIHURE.
CC PDB; 1REI; 17-FEB-84.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Bence-Jones protein; 3D-structure.
CC
CC DOMAIN 1 23
CC TRANS 24 34
CC COMPLEMENTARITY-DETERMINING-1.
CC
CC DOMAIN 35 49
CC TRANS 50 56
CC COMPLEMENTARITY-DETERMINING-2.
CC
CC DOMAIN 57 88
CC TRANS 59 97
CC COMPLEMENTARITY-DETERMINING-3.
CC
CC DOMAIN 98 107
CC TRANS 102 106
CC COMPLEMENTARITY-DETERMINING-4.
CC
CC DISULFID 23 88
CC STRAND 4 7
CC
CC STRAND 10 13
CC TURN 15 16
CC
CC STRAND 19 25
CC TURN 30 31
CC
CC STRAND 33 38
CC TURN 40 41
CC
CC STRAND 45 49
CC TURN 50 52
CC
CC STRAND 53 54
CC TURN 56 57
CC
CC STRAND 60 61
CC TURN 62 67
CC
CC STRAND 68 69
CC TURN 70 75
CC
CC STRAND 80 82
CC TURN 85 90
CC
CC STRAND 98 98
CC TURN 102 106
CC
CC STRAND 108 108
CC NON_TER 108 108
CC
CC SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 68.1%; Score 32; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db :| |||||
90 QYQSLPYT 97

Search completed: March 10, 2003, 16:57:47
Job time : 6.58621 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 11.9483 seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-3
Perfect score: 54
Sequence: 1 RASQDIGSKLY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	88	2	PIR0261
2	42	77.8	106	2	Ig kappa chain V r
3	42	77.8	130	1	Ig kappa chain V r
4	38	70.4	114	2	Ig kappa chain pre
5	37	68.5	106	2	Ig kappa chain pre
6	37	68.5	234	2	Ig kappa chain V r
7	36	66.7	305	2	probable purine nu
8	36	66.7	442	2	sugar binding prot
9	36	66.7	548	2	hypothetical prote
10	35	64.8	95	2	hypothetical prote
11	35	64.8	107	2	Ig kappa chain V r
12	35	64.8	108	2	anti-HIV envelope
13	34	63.0	193	2	Ig kappa chain V r
14	34	63.0	252	2	hypothetical prote
15	34	63.0	269	2	40s ribosomal prot
16	34	63.0	324	2	S62431
17	34	63.0	377	2	spermidine/putresc
18	34	63.0	471	2	probable oxidoredu
19	34	63.0	494	1	hypothetical prote
20	34	63.0	876	2	conserved hypotet
21	34	63.0	886	2	intercellular spre
22	33	61.1	87	2	probable vals prot
23	33	61.1	107	2	valyl-tRNA synthas
24	33	61.1	115	1	Ig light chain V r
25	33	61.1	117	2	Ig kappa chain V r
26	33	61.1	128	2	Ig kappa chain pre
27	33	61.1	129	2	Ig kappa chain V-J
28	33	61.1	129	2	Ig kappa chain pre
29	33	61.1	129	2	Ig kappa chain V r
				2	Ig kappa chain - h
				2	S40332

30	33	61.1	225	2	T03555	hypothetical prote
31	33	61.1	237	2	S65313	probable membrane
32	33	61.1	322	2	S35380	mcs2 protein - fls
33	33	61.1	346	2	T35215	hypothetical prote
34	33	61.1	349	2	D75419	proline dipeptidas
35	33	61.1	366	2	B95876	probable ABC trans
36	33	61.1	375	2	T25089	hypothetical prote
37	33	61.1	415	1	GRECST	sucrose transport
38	33	61.1	415	2	A98034	sucrose transport
39	33	61.1	415	2	B85878	sucrose permease [
40	33	61.1	530	1	KICHPM	pyruvate kinase [E
41	33	61.1	548	2	JC6174	immunodominant 120
42	33	61.1	663	2	S67259	MNE1 protein - yea
43	33	61.1	666	2	F71310	probable periplasm
44	33	61.1	672	2	D81746	type III secretion
45	33	61.1	921	2	F71486	probable yopC/gen

ALIGNMENTS

RESULT 1

PIR0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C:Accession: PIR0261
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J.; Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A:Reference number: PIR0231; MUID:90111618; PMID:2104919
A:Accession: PIR0261
A:Molecule type: mRNA
A:Residues: 1-88 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-5/Region: framework 1
F:16-16/Region: complementarity-determining 1
F:17-31/Region: framework 2
F:32-38/Region: complementarity-determining 2
F:39-70/Region: framework 3
F:71-79/Region: complementarity-determining 3
F:80-88/Region: framework 4

Query Match 77.8%; Score 42; DB 2; Length 88;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
DB 6 RASQDIGSSL 15
|||||||

RESULT 2

PIR0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PIR0260
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J.; Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A:Reference number: PIR0231; MUID:90111618; PMID:2104919
A:Accession: PIR0260
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 77.8%; Score 42; DB 2; Length 106;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
|||||||

Db 24 RASQDIGSSL 33

RESULT 3

KVMSM4

Ig kappa chain precursor V region (MOPC 41) - mouse

N:Contains: Ig kappa chain precursor V region VK41

C:Species: Mus musculus (house mouse)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999

C:Accession: A93211; B93211; A93815; A94239; A01922; A01923

R:Seidman, J.G.; Max, E.E.; Leder, P.

Nature 280, 370-375, 1979

A:Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu

A:Reference number: A93211; MUID:79221900; PMID:111146

A:Accession: A93211

A:Molecule type: DNA

A:Residues: 1-130 <PC41>

A:Accession: B93211

A:Molecule type: DNA

A:Residues: 1-117 <VK41>

A:Cross-references: GB:J00804; GB:J00566; NID:952127; PIDN:CAA24186.1; PID:9575660

A:Note: The sequences were determined from the differentiated gene MOPC 41 and the germ

R:Burstein, Y.; Schechter, I.

Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977

A:Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors

A:Reference number: A93815; MUID:77148916; PMID:403522

A:Accession: A93815

A:Molecule type: protein

A:Residues: 1-33 <BUR>

A:Note: Met-3 is apparently used as an alternative initiator in 25% of the chains

R:Gray, W.R.; Dreyer, W.J.; Hood, L.

Science 155, 465-467, 1967

A:Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.

A:Reference number: A94239; MUID:67056897; PMID:4162931

A:Accession: A94239

A:Molecule type: protein

A:Residues: 23-49, 'B', '51-53, 'LSB', '57-58, 'ZZ', '61-62, 'BZ', '65-76, 'B', '78-108, 110-130 <GRA>

A:Experimental source: Bence Jones protein MOPC 41

C:Genetics:

A:Introns: 19/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region: immunoglobulin homology

C:Keywords: alternative initiators; heterotetramer; immunoglobulin

F:1-22/Domain: signal sequence #status experimental <SIG>

F:3-22/Domain: signal sequence #status experimental <SIG>

F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>

F:38-112/Domain: immunoglobulin homology <IMM>

F:45-110/Disulfide bonds: #status predicted

Query Match 77.8%; Score 42; DB 1; Length 130;

Best Local Similarity 90.0%; Pred. No. 0.31;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
|||||||

Db 46 RASQDIGSSL 55

RESULT 4

S00996

Ig kappa chain precursor V region (A10) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
C:Accession: S00996

R:Straubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.

Biol. Chem. Hoppe-Seyler 369, 601-607, 1988

A:Title: Two unusual human immunoglobulin V-kappa genes.

A:Reference number: S00996; MUID:89134397; PMID:2852016

A:Accession: S00996

A:Molecule type: DNA

A:Residues: 1-114 <STR>

A:Cross-references: EMBL:M27750; NID:q185914; PIDN:AAA58912.1; PID:9553479

A:Note: this sequence was determined from the germline gene

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-114/Product: Ig kappa chain V region #status predicted <MAT>

F:42-107/Disulfide bonds: #status predicted

Query Match 70.4%; Score 38; DB 2; Length 114;

Best Local Similarity 72.7%; Pred. No. 1.9;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
|||||||

Db 43 RASQSIGSSLH 53

RESULT 5

PL0259

Ig kappa chain V region (anti-DNA, DPL1VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0259

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 285-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0259

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 68.5%; Score 37; DB 2; Length 106;

Best Local Similarity 80.0%; Pred. No. 2.8;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
|||||||

Db 24 RASQDIGRSL 33

RESULT 6

S38083

probable purine nucleotide-binding protein YPT52 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YKR014C

C:Species: Saccharomyces cerevisiae

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999

C:Accession: S38083

R:Duesterhoeft, A.; Moestl, D.; Poehlmann, R.; Philippsen, P.

submitted to the Protein Sequence Database, March 1994

A:Reference number: S37811

A:Accession: S38083

A:Molecule type: DNA

A:Residues: 1-234 <DUE>
A:Cross-references: EMBL:Z28239; NID:9486428; PIDN:CAA82086.1; PID:9486429; MIPS:YKR014C
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:YPT52
A:Cross-references: SGD:S0001722; MIPS:YKR014C
A:Map position: 11R
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; P-loop; purine nucleotide binding
F:10-17/Region: nucleotide-binding motif A (P-loop)
F:125-128/Region: GTP-binding NKXD motif
F:175-177/Region: GTP-binding SAK/L motif
F:16/Binding site: ATP/GTP (lys) #status predicted

Query Match 68.5%; Score 37; DB 2; Length 234;
Best Local Similarity 87.5%; Pred. No. 6.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QDIGSKLY 11
||| |||
Db 187 ODIGEKLY 194

RESULT 7
AF0305
sugar binding protein precursor [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0305
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0305
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC91306.1; PID:g15980495; GSPDB:GN00175
C:Genetics:
A:Gene: rbsB

Query Match 66.7%; Score 36; DB 2; Length 305;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
:|:||||:|
Db 52 QANDIGAKVY 62

RESULT 8
E71523
hypothetical protein CT372 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: E71523
R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: AY1570; MUID:99000809; PMID:9784136
A:Accession: E71523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <RAN>
A:Cross-references: GB:AE001310; GB:AE001273; NID:g3328789; PIDN:AAC67968.1; PID:g332879
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT372

Query Match 66.7%; Score 36; DB 2; Length 442;
Best Local Similarity 80.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQDIGSKLY 11
||| | |||
Db 327 ASQHISSKLY 336

RESULT 9
A86385
hypothetical protein F2J7.18 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: A86385
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86385
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <STO>
A:Cross-references: GB:AE005172; NID:g10092315; PIDN:AAG12726.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 548;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
:| | |||:|
Db 48 KALYDIGAKLY 58

RESULT 10
PH0867
Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0867
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A:Reference number: PH0862; MUID:92078875; PMID:1660528
A:Accession: PH0867
A:Molecule type: DNA
A:Residues: 1-95 <MAN>
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-95/Region: complementarity-determining 3

Query Match 64.8%; Score 35; DB 2; Length 95;
Best Local Similarity 72.7%; Pred. No. 6.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGSKLY 11
||| | ||| :
Db 24 RASQSIGSFLLH 34

RESULT 11

I69017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (f
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I69017
R:Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A:Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A:Reference number: I54563; MUID:95237884; PMID:7721339
A:Accession: I69017
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-107 <RES>
A:Cross-references: GB:S77140; NID:g913352; PIDN:AA34102.1; PID:g913353
C:Genetics:
A:Gene: Ig vkappa
A:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 35; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKL 10
||| |||||
DB 24 RASHDIGSYL 33

RESULT 12

C30502
Ig kappa chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: C30502
R:Ellat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mid
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: C30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <EIL>
A:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 35; DB 2; Length 108;
Best Local Similarity 63.6%; Pred. No. 7.5;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
|||| |||||
DB 24 RASQSIGSLH 34

RESULT 13

H82028
hypothetical protein NMA0330 [imported] - Neisseria meningitidis (strain 22491 serogroup
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: H82028
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: H82028
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <PAR>

A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83635.1; PID:g737
A:Experimental source: serogroup A, strain 22491
C:Genetics:
A:Gene: NMA0330

Query Match 63.0%; Score 34; DB 2; Length 193;
Best Local Similarity 63.6%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGSKLY 11
||| |||||
DB 63 RAAQRRGAKLY 73

RESULT 14

S62431
40S ribosomal protein s3ae (S1) - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: protein SPAC1366.02c
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 10-Dec-1999
C:Accession: S62431; T37637
R:Odell, C.; Bowman, S.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62430
A:Accession: S62431
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <ODE>
A:Cross-references: EMBL:Z54308; NID:g1008985; PIDN:CAA91095.1; PID:g1008987
R:Odell, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21734
A:Accession: T37637
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-252 <OD2>
A:Cross-references: EMBL:Z54308; PIDN:CAA91095.1; GSPDB:GN00066; SPDB:SPAC1366.02c
A:Experimental source: strain 972h-; cosmid c1366
C:Genetics:
A:Gene: rps1-1
A:Map position: 1L
C:Superfamily: rat ribosomal protein S3a
C:Keywords: protein biosynthesis; ribosome

Query Match 63.0%; Score 34; DB 2; Length 252;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SQDIGSKL 10
||| |||||
DB 235 SQDVGSKV 242

RESULT 15

H70179
spermidine/putrescine ABC transporter, permease protein (potB) homolog - Lyme disease
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 24-Sep-1999
C:Accession: H70179
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: H70179
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <KLE>
A:Cross-references: GB:AE001165; GB:AE000783; NID:g2688561; PIDN:AAB91526.1; PID:g268
A:Experimental source: strain B31
C:Superfamily: spermidine/putrescine transport system permease protein potB

Query Match 63.0%; Score 34; DB 2; Length 269;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASQDIGSKLY 11
| | | | : | : : :
Db 171 ASQDLGARMW 180

Search completed: March 10, 2003, 17:01:22
Job time : 13.9483 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 7.60345 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-4
Perfect score: 31
Sequence: 1 ATSSLDS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	88	2	Ig kappa chain V r
2	31	100.0	106	2	Ig kappa chain V r
3	31	100.0	106	2	Ig kappa chain V r
4	31	100.0	130	1	Ig kappa chain pre
5	31	100.0	131	2	hypothetical prote
6	31	100.0	320	2	ABC transporter AT
7	31	100.0	548	2	ABC transporter AT
8	31	100.0	555	2	hypothetical prote
9	31	100.0	589	2	ABC transporter (A
10	31	100.0	589	2	hypothetical prote
11	31	100.0	600	2	hypothetical prote
12	31	100.0	600	2	ATP-binding transp
13	31	100.0	604	2	ATP-binding transp
14	31	100.0	604	2	msbA-like sacchari
15	31	100.0	1025	2	multidrug resistan
16	31	100.0	1419	1	multidrug resistan
17	28	90.3	327	2	ABC transporter, A
18	28	90.3	327	2	ABC transporter, A
19	28	90.3	428	2	zinc finger protei
20	28	90.3	534	2	ABC-type transport
21	28	90.3	546	2	ATP-binding protei
22	28	90.3	571	2	pepT protein - Sta
23	28	90.3	575	2	ABC transporter (A
24	28	90.3	575	2	ABC transporter (A
25	28	90.3	578	2	ABC transporter (A
26	28	90.3	584	2	hypothetical prote
27	28	90.3	587	2	probable ABC trans
28	28	90.3	587	2	hypothetical prote
29	28	90.3	588	2	ABC transporter, A

30	28	90.3	607	2	A35391	hetA protein - Ana
31	28	90.3	607	2	AD2160	heterocyst differe
32	28	90.3	609	2	G71731	mitochondrial tran
33	28	90.3	610	2	H83243	probable ATP-bindi
34	28	90.3	611	2	H82351	probable hemolysin
35	28	90.3	614	2	A64180	probable ATP-bindi
36	28	90.3	616	2	AI2851	hypothetical prote
37	28	90.3	618	2	B81796	probable ABC trans
38	28	90.3	618	2	A81218	hypothetical prote
39	28	90.3	619	2	F82391	ABC transporter, A
40	28	90.3	622	2	AB3311	ABC transporter AT
41	28	90.3	626	2	AI3310	ABC transporter AT
42	28	90.3	627	2	AH2851	hypothetical prote
43	28	90.3	633	2	T27215	hypothetical prote
44	28	90.3	633	2	G97628	ATP-binding protei
45	28	90.3	634	2	T48418	ABC transporter-li

ALIGNMENTS

RESULT 1

PL0261

Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997

C:Accession: PL0261

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0261

A:Residues: 1-88 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-5/Region: framework 1

F:16-16/Region: complementarity-determining 1

F:17-31/Region: framework 2

F:32-38/Region: complementarity-determining 2

F:39-70/Region: framework 3

F:71-79/Region: complementarity-determining 3

F:80-88/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSLDS 7
Db 32 ATSSLDS 38

RESULT 2

PL0260

Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment) ;

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0260

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0260

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: complementarity-determining 2

F:50-56/Region: framework 2

F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 50 ATSSLDS 56

RESULT 3

PL0259

Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C:Accession: PL0259

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.2.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171.1:265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0259

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 106;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 50 ATSSLDS 56

RESULT 4

KVMSM4

Ig kappa chain precursor V region (MOPC 41) - mouse

N:Contains: Ig kappa chain precursor V region VK41

C:Species: Mus musculus (house mouse)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999

C:Accession: A93211; B93211; A93815; A94239; A01922; A01923

R:Seidman, J.G.; Max, E.E.; Leder, P.

Nature 280, 370-375, 1979

A:Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu

A:Reference number: A93211; MUID:79221900; PMID:111146

A:Accession: A93211

A:Molecule type: DNA

A:Residues: 1-130 <PC41>

A:Accession: B93211

A:Molecule type: DNA

A:Residues: 1-117 <VK41>

A:Cross-references: GB:J00804; GB:J00566; NID:q52127; PIDN:CAA24186.1; PID:q575660

A>Note: The sequences were determined from the differentiated gene MOPC 41 and the germ

R:Burstein, Y.; Schechter, I.

Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977

A:Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors

A:Reference number: A93815; MUID:77148916; PMID:403522

A:Accession: A93815

A:Molecule type: protein

A:Residues: 1-33 <BUR>

A>Note: Met-3 is apparently used as an alternative initiator in 25% of the chains

R:Gray, W.R.; Dreyer, W.J.; Hood, L.

Science 155, 465-467, 1967

A:Title: Mechanism of antibody synthesis: size differences between mouse kappa chains

A:Reference number: A94239; MUID:67056897; PMID:4162931

A:Accession: A94239

A:Molecule type: protein

A:Residues: 23-49, 'B', '51-53, 'LSB', 57-58, '22', '61-62, 'BZ', '65-76, 'B', '78-108, 110-130 <GRA

A:Experimental source: Bence Jones protein MOPC 41

C:Genetics:

A:Introns: 19/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: alternative initiators; heterotetramer; immunoglobulin

F:1-22/Domain: signal sequence #status experimental <SIG1>

F:3-22/Domain: signal sequence #status experimental <SIG2>

F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>

F:38-112/Domain: immunoglobulin homology <IMM>

F:45-110/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 130;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 72 ATSSLDS 78

RESULT 5

E97737

hypothetical protein RC0301 [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 19-Jul-2002

C:Accession: E97737

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: E97737

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-131 <KUR>

A:Cross-references: GB:AE006914; PIDN:AAL02839.1; PID:gl15619360; GSPDB:GN00173

C:Genetics:

A:Gene: RC0301

C:Superfamily: multidrug resistance protein; ATP-binding cassette homology

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 131;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 62 ATSSLDS 68

RESULT 6

AI3469

ABC transporter ATP-binding protein BME11743 [imported] - Brucella melitensis (strain

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AI3469

R:DelVecchio, V.G.; Kapatal, R.J.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit

A:Reference number: AD3252; PMID:11756688

A:Accession: AI3469

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-320 <KUR>

A:Cross-references: GB:AE008917; PIDN:AAL52924.1; PID:gl17983771; GSPDB:GN00190

A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME11743
 A:Map position: 1

Query Match 100.0%; Score 31; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

Db 235 ATSSLS 241

RESULT 7

F71732
 ABC transporter ATP-binding protein (abcT3) RP214 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
 C:Accession: F71732
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, U.
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893
 A:Accession: F71732
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-548 <AND>
 A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAAL4677.1; PID:e134252

A:Experimental source: strain Madrid E

C:Genetics:
 A:Gene: abcT3; RP214
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
 C:Keywords: ATP
 F:323-517/Domain: ATP-binding cassette homology <ABC>

Query Match 100.0%; Score 31; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

Db 470 ATSSLS 476

RESULT 8

S63137
 hypothetical protein YNL182c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein NI636
 C:Species: Saccharomyces cerevisiae
 C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
 C:Accession: S63137
 R:Obermaier, B.; Piravandi, E.; Rinke, M.; Domdey, H.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63122
 A:Accession: S63137
 A:Molecule type: DNA
 A:Residues: 1-555 <OBE>
 A:Cross-references: EMBL:Z71458; NID:g1302165; PID:e239555; PID:g1302166; GSPDB:GN00014;
 A:Experimental source: strain S288
 C:Genetics:
 A:Gene: MIPS:YNL182C
 A:Cross-references: SGD:S0005126
 A:Map position: 14L

Query Match 100.0%; Score 31; DB 2; Length 555;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

Db 506 ATSSLS 512

RESULT 9

D70031

ABC transporter (ATP-binding protein) homolog yvcc - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
 C:Accession: D70031
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiya
 T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: D70031

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-589 <KUN>

A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15487.1; PID:g26359

A:Experimental source: strain 168

C:Genetics:

A:Gene: yvcc

C:Superfamily: Escherichia coli ABC transporter mdia; ATP-binding cassette homology

C:Keywords: ATP; nucleotide binding; P-loop

F:357-552/Domain: ATP-binding cassette homology <ABC>

F:374-381/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 31; DB 2; Length 589;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

Db 505 ATSSLS 511

RESULT 10

F97735
 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7)
 C:Species: Rickettsia conorii
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
 C:Accession: F97735
 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
 Science 293, 2093-2098, 2001
 A:Title: Mechanisms of evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: F97735

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-589 <KUR>

A:Cross-references: GB:AE006914; PIDN:AAL02824.1; PID:g15619343; GSPDB:GN00173

C:Genetics:

A:Gene: abcT3

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 100.0%; Score 31; DB 2; Length 589;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLS 7

Db 511 ATSSLS 517

RESULT 11

AD3138
 A:Reference number: S60182
 A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <SEC>
 A:Cross-references: EMBL:Z50189; NID:gl143532; PIDN:CAA90568.1; PID:el91488; PID:gl14
 A:Note: It is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the init
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
 A:Map position: linear chromosome
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AD3138
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-600 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AA45522.1; PID:gl17743233; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 100.0%; Score 31; DB 2; Length 600;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 517 ATSSLDS 523

RESULT 12

H98149
 A:Reference number: S60182
 A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-600 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK88722.1; PID:gl15158459; GSPDB:GN00170
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: AGR_L_309
 A:Map position: linear chromosome

Query Match 100.0%; Score 31; DB 2; Length 600;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 517 ATSSLDS 523

RESULT 13

S60182
 A:Reference number: S60182
 A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-600 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK88722.1; PID:gl15158459; GSPDB:GN00170
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: AGR_L_309
 A:Map position: linear chromosome

Query Match 100.0%; Score 31; DB 2; Length 600;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Reference number: S60181; MUID:96133689; PMID:8544814

A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <SEC>
 A:Cross-references: EMBL:Z50189; NID:gl143532; PIDN:CAA90568.1; PID:el91488; PID:gl14
 A:Note: It is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the init
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
 A:Map position: linear chromosome
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AD3138
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-600 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AA45522.1; PID:gl17743233; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 100.0%; Score 31; DB 2; Length 604;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 518 ATSSLDS 524

RESULT 14

H95974
 A:Reference number: S60182
 A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49464.1; PID:gl15140950; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
 pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: exsA; SMB20941
 A:Genome: plasmid

Query Match 100.0%; Score 31; DB 2; Length 604;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSLDS 7

|||||||

Db 518 ATSSLDS 524

RESULT 15

T18376
 A:Reference number: S60182
 A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <SEC>
 A:Cross-references: EMBL:Z50189; NID:gl143532; PIDN:CAA90568.1; PID:el91488; PID:gl14
 A:Note: It is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the init
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
 A:Map position: linear chromosome
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AD3138
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-600 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AA45522.1; PID:gl17743233; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

A:Reference number: S60182; MUID:96133689; PMID:8544814

A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <SEC>
 A:Cross-references: EMBL:Z50189; NID:gl143532; PIDN:CAA90568.1; PID:el91488; PID:gl14
 A:Note: It is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the init
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

A:Reference number: S60182; MUID:96133689; PMID:8544814

A:Accession: S60182
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <SEC>
 A:Cross-references: EMBL:Z50189; NID:gl143532; PIDN:CAA90568.1; PID:el91488; PID:gl14
 A:Note: It is uncertain whether Met-1 (ATG), Val-29 (GTG) or Met-74 (ATG) is the init
 C:Genetics:
 A:Gene: exsA
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

A:Molecule type: DNA
A:Residues: 1-1025 <RUB>
A:Cross-references: EMBL:U04640; NID:g439853; PID:g439854; PIDN:AAA21513.1
C:Genetics:
A:Gene: mdr2

Query Match 100.0%; Score 31; DB 2; Length 1025;
Best Local Similarity 100.0%; Pred. NO. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSIDS 7
|
Db 851 ATSSIDS 857

Search completed: March 10, 2003, 17:01:23
Job time : 8.60345 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 9.77586 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-5
Perfect score: 47
Sequence: 1 LQYASSPYT 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	98	PH1062	Ig light chain V r
2	47	100.0	101	C28840	Ig kappa chain V r
3	47	100.0	101	B28840	Ig kappa chain V r
4	43	91.5	92	D28840	Ig kappa chain V r
5	42	89.4	88	PL0261	Ig kappa chain V r
6	42	89.4	106	PL0260	Ig kappa chain V r
7	42	89.4	130	KVMSM4	Ig kappa chain pre
8	40	85.1	321	S57530	carboxyl esterase
9	39	83.0	91	S67940	Ig kappa chain V r
10	39	83.0	92	S37513	Ig kappa chain V r
11	39	83.0	106	PL0259	Ig kappa chain V r
12	39	83.0	109	A30608	Ig kappa chain V-I
13	39	83.0	109	H30601	Ig kappa chain V-I
14	37	78.7	128	K3HU41	Ig kappa chain pre
15	36	76.6	106	PL0262	Ig kappa chain V r
16	36	76.6	282	G64120	phot protein - Hae
17	36	76.6	947	G86557	polymorphic membra
18	36	76.6	947	D27067	polymorphic membra
19	35	74.5	92	S37524	Ig kappa chain V r
20	35	74.5	108	K3HUB6	Ig kappa chain V-I
21	35	74.5	109	G30607	Ig kappa chain V-I
22	35	74.5	117	KVMS3B	Ig kappa chain pre
23	35	74.5	536	A99283	hypothetical prote
24	35	74.5	619	B97475	hypothetical prote
25	35	74.5	619	AF2693	conserved hypothet
26	35	74.5	761	T33816	hypothetical prote
27	35	74.5	1290	A56493	leukocyte common a
28	35	74.5	1897	1 TDHUK	leukocyte antigen-
29	35	74.5	1898	2 S46216	leukocyte antigen-

Ig kappa chain V r
Ig kappa chain V r
IgA kappa rheumato
Ig kappa chain V-I
Ig kappa chain V r
Ig kappa chain pre
hypothetical prote
gene Cx protein -
hypothetical prote
Ig kappa chain pre
ABC transporter ph
dcuc protein - Esc
c4-dicarboxylate a
transport of dicar
c4-dicarboxylate a
hypothetical prote

ALIGNMENTS

RESULT 1
PH1062

Ig light chain V region (clone 202.105) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1062
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1062

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-98 <full>

A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
DB 89 LQYASSPYT 97

RESULT 2

C28840

Ig kappa chain V region (HP22) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jan-2000

C:Accession: C28840; J25114

R:Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.

EMBO J. 4, 3661-3688, 1985

A:Title: The idiotypic network and the internal image: possible regulation of a germ-
A:Reference number: A91028; MUID:86136012; PMID:3937730

A:Accession: C28840

A:Molecule type: mRNA

A:Residues: 1-101 <OLL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:10-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 47; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
DB 83 LQYASSPYT 91

```

RESULT 3
B28840
Ig kappa chain V region (HP27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jan-2000
C:Accession: B28840; J25114
R:Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A:Title: The idiotypic network and the internal image: possible regulation of a germ-line
A:Reference number: A91028; MUID:86136012; PMID:3937730
A:Accession: B28840
A:Molecule type: mRNA
A:Residues: 1-101 <OLL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 47; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 83 LQYASSPYT 91

RESULT 4
D28840
Ig kappa chain V region (HP29) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jan-2000
C:Accession: D28840; K25114
R:Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A:Title: The idiotypic network and the internal image: possible regulation of a germ-line
A:Reference number: A91028; MUID:86136012; PMID:3937730
A:Accession: D28840
A:Molecule type: mRNA
A:Residues: 1-92 <OLL>
A:Cross-references: GB:X03384; NID:g52157; PIDN:CAA27111.1; PID:g52158
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-75/Domain: immunoglobulin homology <IMM>

Query Match 91.5%; Score 43; DB 2; Length 92;
Best Local Similarity 88.9%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 74 LQYASSPYT 82

RESULT 5
PL0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C:Accession: PL0261
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0261
A:Molecule type: mRNA
A:Residues: 1-88 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-5/Region: framework 1
F:6-16/Region: complementarity-determining 1
F:17-31/Region: framework 2

```

```

F:32-38/Region: complementarity-determining 2
F:39-70/Region: framework 3
F:71-79/Region: complementarity-determining 3
F:80-88/Region: framework 4

Query Match 89.4%; Score 42; DB 2; Length 88;
Best Local Similarity 88.9%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 71 LQYASSPYT 79

RESULT 6
PL0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0260
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0260
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 89.4%; Score 42; DB 2; Length 106;
Best Local Similarity 88.9%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQYASSPYT 9
Db 89 LQYASSPYT 97

RESULT 7
KVNSM4
Ig kappa chain precursor V region (MOPC 41) - mouse
N:Contains: Ig kappa chain precursor V region VK41
C:Species: Mus musculus (house mouse)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999
C:Accession: A93211; B93211; A93815; A94239; A01922; A01923
R:Seidman, J.G.; Max, E.E.; Leder, P.
Nature 280, 370-375, 1979
A:Title: A kappa-immunoglobulin gene is formed by site-specific recombination without
A:Reference number: A93211; MUID:79221900; PMID:111146
A:Accession: A93211
A:Molecule type: DNA
A:Residues: 1-130 <PC41>
A:Accession: B93211
A:Molecule type: DNA
A:Residues: 1-117 <VK41>
A:Cross-references: GB:V00804; GB:J00566; NID:g52127; PIDN:CAA24186.1; PID:g575660
A>Note: the sequences were determined from the differentiated gene MOPC 41 and the ge
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
R:Burstein, Y.; Schechter, I.
A:Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precurs
A:Reference number: A93815; MUID:77148916; PMID:403522
A:Accession: A93815
A:Molecule type: protein
A:Residues: 1-33 <BUR>

```


A:Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
R:Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A:Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.
A:Reference number: A94239; MUID:67056897; PMID:4162931
A:Accession: A94239
A:Molecule type: protein
A:Residues: 23-49,'B','51-53','LSB','57-58','22','61-62','B2','65-76','B','78-108,110-130 <GRA>
A:Experimental source: Bence Jones protein MOPC 41
C:Genetics:
A:Introns: 19/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: alternative initiators; heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status experimental <SIG1>
F:3-22/Domain: signal sequence #status experimental <SIG2>
F:23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F:38-112/Domain: immunoglobulin homology <IMM>
F:45-110/Disulfide bonds: #status predicted

Query Match 89.4%; Score 42; DB 1; Length 130;
Best Local Similarity 88.9%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQYASSPYT 9
|||:||||:|
Db 111 LQYASSPWT 119

RESULT 8
S57530
carboxyl esterase - Acinetobacter calcoaceticus
C:Species: Acinetobacter calcoaceticus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S57530
R:Kok, R.G.; Bart, A.; Hellingwerf, K.J.
submitted to the EMBL Data Library, June 1995
A:Description: Characterization of the estBR operon of Acinetobacter calcoaceticus BD413
A:Reference number: S57529
A:Accession: S57530
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-321 <KOK>
A:Cross-references: EMBL:X88895
C:Genetics:
A:Start codon: GTG
C:Superfamily: carboxyl esterase

Query Match 85.1%; Score 40; DB 1; Length 321;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQYASSPYT 9
|||:|||||
Db 14 LQFSSSPYT 22

RESULT 9
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C:Accession: S67940
R:Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A:Title: Cloning of a human autoimmune response: preparation and sequencing of a human a
A:Reference number: S67940; MUID:92314301; PMID:1617110
A:Accession: S67940
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <HEX>
A:Cross-references: EMBL:X73852

C:Superfamily: immunoglobulin V region; immunoglobulin homology
Query Match 83.0%; Score 39; DB 2; Length 91;
Best Local Similarity 87.5%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYASSPYT 9
|||:|||||
Db 72 QYGSSPYT 79

RESULT 10
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37513
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37501
A:Accession: S37513
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81352.1; PID:g405669
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 83.0%; Score 39; DB 2; Length 92;
Best Local Similarity 87.5%; Pred. No. 0.82;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYASSPYT 9
|||:|||||
Db 74 QYGSSPYT 81

RESULT 11
PL0259
Ig kappa chain V region (anti-DNA, DP1LVK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0259
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:9011618; PMID:2104919
A:Accession: PL0259
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 83.0%; Score 39; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 0.95;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQYASSPYT 9
|||:||||:|
Db 89 LQYATSPWT 97

RESULT 12
A30608

```

Ig kappa chain V-III region (Son) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C:Accession: A30608
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: A30608
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <CON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 39; DB 2; Length 109;
Best Local Similarity 87.5%; Pred. No. 0.98;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 91 QYGSSPYT 98
||| |||||

RESULT 13
H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C:Accession: H30601; E30601
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: H30601
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GONI>
A:Accession: E30601
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <CON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 39; DB 2; Length 109;
Best Local Similarity 87.5%; Pred. No. 0.98;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 91 QYGSSPYT 98
||| |||||

RESULT 14
K3H041
Ig kappa chain precursor V-III region (IARC/BL41) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C:Accession: A01899
R:Klobeck, H.G.; Meindl, A.; Combrinato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852; PMID:2997711
A:Accession: A01899
A:Molecule type: DNA
A:Residues: 1-128 <KLO>
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266

```

```

A:Map position: 2p12-2p11
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-128/Product: Ig kappa chain V-III region (IARC/BL41) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:55-69/Region: framework 2
F:77-108/Region: complementarity-determining 2
F:109-117/Region: complementarity-determining 3
F:118-128/Region: framework 4
F:43-108/Disulfide bonds: #status predicted

Query Match 78.7%; Score 37; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 3;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYASSPYT 9
Db 110 QYSTSPYT 117
||| |||||

RESULT 15
PL0262
Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0262
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0262
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 76.6%; Score 36; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYASSPYT 9
Db 89 QYASYPWT 97
||| |||||

Search completed: March 10, 2003, 17:01:24
Job time : 10.7759 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 9.82759 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	82.8	117	2	US-08-814-806-4
2	48	82.8	142	2	US-08-678-194-8
3	48	82.8	142	4	US-08-890-011-8
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5	47	81.0	123	1	US-08-497-312-15
6	47	81.0	123	1	US-08-497-312-17
7	47	81.0	123	2	US-08-560-558E-28
8	46	79.3	110	4	US-09-214-095D-86
9	46	79.3	116	2	US-08-672-345C-106
10	46	79.3	116	2	US-08-672-345C-105
11	46	79.3	116	4	US-09-214-095D-90
12	45	77.6	115	2	US-08-672-345C-18
13	45	77.6	115	2	US-08-672-345C-108
14	45	77.6	115	4	US-09-214-095D-18
15	45	77.6	115	4	US-09-214-095D-98
16	45	77.6	118	1	US-08-477-877B-93
17	45	77.6	118	2	US-08-472-281A-93
18	45	77.6	118	2	US-08-477-898B-93
19	45	77.6	137	1	US-08-477-877B-96
20	45	77.6	137	2	US-08-472-281A-96
21	45	77.6	137	2	US-08-477-898B-96
22	45	77.6	138	3	US-08-603-024-2
23	45	77.6	139	1	US-08-253-877C-8
24	45	77.6	139	1	US-08-253-877C-19
25	45	77.6	139	2	US-08-452-164A-8
26	45	77.6	139	2	US-08-452-164A-19
27	45	77.6	139	3	US-08-603-024-18

Sequence 41, Appl
Sequence 41, Appl
Sequence 27, Appl
Sequence 100, App
Sequence 102, App
Sequence 112, App
Sequence 27, Appl
Sequence 100, App
Sequence 102, App
Sequence 112, App
Sequence 27, Appl
Sequence 100, App
Sequence 102, App
Sequence 112, App
Sequence 7, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 23, Appl
Sequence 16, Appl
Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-814-806-4
; Sequence 4, Application US/08814806
; Patent No. 5986065
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; APPLICANT: Jiao, Jin-an
; APPLICANT: Esperanza, Nieves
; APPLICANT: Lawrence, Luepschen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DiKe, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,806
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

US-08-814-806-4

Query Match 82.8%; Score 48; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.49;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSTDYFIY 10
| | | | | : |
Db 26 GYSTDYINV 35

RESULT 2

US-08-678-194-8
; Sequence 8, Application US/08678194
; Patent No. 5922845

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; TITLE OF INVENTION: Comprised of Anti-Fc(SYMBOL 97 \f "Symbol") Receptor Antibodies

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194

; FILING DATE: July 11, 1996

; PRIOR APPLICATION DATA: No. 5922845e

; APPLICATION NUMBER: US

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Beth A. Arnold

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: NX1-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 142 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-678-194-8

Query Match 82.8%; Score 48; DB 2; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSTDYFIY 10
| | | | | : |
Db 45 GYSTDYIIF 54

RESULT 3

US-08-890-011-8

; Sequence 8, Application US/08890011
; Patent No. 6193966

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; APPLICANT: Graziano, Robert

; APPLICANT: Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; TITLE OF INVENTION: Comprised of Anti-Fc
; TITLE OF INVENTION: {SYMBOL 97 \f "Symbol"} Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/890,011

; FILING DATE: July 9, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/678,194

; FILING DATE: July 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Jane E. Remillard

; REGISTRATION NUMBER: 38,872

; REFERENCE/DOCKET NUMBER: NX1-064CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 142 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-890-011-8

Query Match 82.8%; Score 48; DB 4; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSTDYFIY 10
| | | | | : |
Db 45 GYSTDYIIF 54

RESULT 4

US-09-262-724-8

; Sequence 8, Application US/09262724
; Patent No. 6303755

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; APPLICANT: Graziano, Robert

; APPLICANT: Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; TITLE OF INVENTION: Comprised of Anti-Fc(SYMBOL 97 \f "Symbol")

; TITLE OF INVENTION: Receptor Antibodies

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,724

; FILING DATE: 04-Mar-1999

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/678,194
FILING DATE: July 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Beth A. Arnold
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 82.8%; Score 48; DB 4; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
DB 45 GYSFTDYIIF 54

RESULT 5

US-08-497-312-15
Sequence 15, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94

FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:

NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 801/532-1922

TELEFAX: 801/531-9168

TELEX: 388961 1PM04UT

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-08-497-312-15

Query Match 81.0%; Score 47; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
DB 26 GYTFTNYIY 35

RESULT 6

US-08-497-312-17
Sequence 17, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94

FILING DATE: 30-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: BOND, LAURENCE B.

REGISTRATION NUMBER: 30,549

REFERENCE/DOCKET NUMBER: 2629US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 801/532-1922

TELEFAX: 801/531-9168

TELEX: 388961 1PM04UT

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-08-497-312-17

Query Match 81.0%; Score 47; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
DB 26 GYTFTNYIY 35

RESULT 7

US-08-560-558E-28
Sequence 28, Application US/08560558E
Patent No. 5891996
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Humanized and chimeric monoclonal

TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor

TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
STREET: P.O. Box 2250
CITY: Salt Lake City
STATE: Utah
COUNTRY: United States of America
ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: Wordperfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E
FILING DATE: NO. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2720US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-560-558E-28

Query Match 81.0%; Score 47; DB 2; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSTDYFIY 10
|:|:|:|:|:
Db 26 GYFTNYIY 35

RESULT 8
US-09-214-095D-86
Sequence 86, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 86
LENGTH: 110
TYPE: PRT
ORGANISM: Murine
US-09-214-095D-86

Query Match 79.3%; Score 46; DB 4; Length 110;
Best Local Similarity 80.0%; Pred. No. 0.97;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSTDYFIY 10
|:|:|:|:|:
Db 20 GYSTDYNNY 29

RESULT 9
US-08-672-345C-105
Sequence 105, Application US/08672345C
Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry, Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-672-345C-105

Query Match 79.3%; Score 46; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSTDYFIY 10
|:|:|:|:|:
Db 26 GYSTDYNNY 35

RESULT 10
US-08-672-345C-106
Sequence 106, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry, Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-106

Query Match 79.3%; Score 46; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 26 GYSFTDYNMY 35

RESULT 11

US-09-214-095D-90
; Sequence 90, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-90

Query Match 79.3%; Score 46; DB 4; Length 116;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 26 GYSFTDYNMY 35

RESULT 12

US-08-672-345C-18
; Sequence 18, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-18

Query Match 77.6%; Score 45; DB 2; Length 115;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 25 GYTFTYYIY 34

RESULT 13

US-08-672-345C-108
; Sequence 108, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-672-345C-108

Query Match 77.6%; Score 45; DB 2; Length 115;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 25 GYTFTYYIY 34

RESULT 14
US-09-214-095D-18
; Sequence 18, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-18

Query Match 77.6%; Score 45; DB 4; Length 115;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTDYFIY 10
||:|:|:|:
Db 25 GYFTTYVIY 34

RESULT 15
US-09-214-095D-98
; Sequence 98, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-98

Query Match 77.6%; Score 45; DB 4; Length 115;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTDYFIY 10
||:|:|:|:
Db 25 GYFTTYVIY 34

Search completed: March 10, 2003, 17:02:32
Job time : 10.8276 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 16.7069 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PC1US_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	76.3	237	2	US-08-468-252-5 Sequence 5, Appli
2	74	76.3	237	3	US-08-668-706B-5 Sequence 5, Appli
3	74	76.3	237	5	PCR-US95-10740-5 Sequence 5, Appli
4	71	73.2	17	1	US-08-137-117D-144 Sequence 144, App
5	71	73.2	17	2	US-08-436-717-144 Sequence 144, App
6	71	73.2	108	2	US-08-888-366-6 Sequence 6, Appli
7	71	73.2	116	2	US-08-561-521-41 Sequence 41, Appl
8	71	73.2	116	5	PCR-US95-01219-41 Sequence 41, Appl
9	71	73.2	135	1	US-08-137-117D-27 Sequence 27, Appl
10	71	73.2	135	1	US-08-137-117D-100 Sequence 100, App
11	71	73.2	135	1	US-08-137-117D-102 Sequence 102, App
12	71	73.2	135	1	US-08-137-117D-112 Sequence 112, App
13	71	73.2	135	2	US-08-436-717-27 Sequence 27, Appl
14	71	73.2	135	2	US-08-436-717-100 Sequence 100, App
15	71	73.2	135	2	US-08-436-717-102 Sequence 102, App
16	71	73.2	135	2	US-08-436-717-112 Sequence 112, App
17	70	72.2	119	1	US-07-634-278-64 Sequence 64, Appl
18	70	72.2	119	1	US-07-634-278-65 Sequence 65, Appl
19	70	72.2	119	1	US-07-634-278-89 Sequence 89, Appl
20	70	72.2	119	1	US-08-477-728-64 Sequence 64, Appl
21	70	72.2	119	1	US-08-477-728-65 Sequence 65, Appl
22	70	72.2	119	1	US-08-477-728-89 Sequence 89, Appl
23	70	72.2	119	1	US-08-474-040-64 Sequence 64, Appl
24	70	72.2	119	1	US-08-474-040-65 Sequence 65, Appl
25	70	72.2	119	1	US-08-474-040-89 Sequence 89, Appl
26	70	72.2	119	1	US-08-487-200-64 Sequence 64, Appl
27	70	72.2	119	1	US-08-487-200-65 Sequence 65, Appl

28	70	72.2	119	1	US-08-487-200-89	Sequence 89, Appl
29	70	72.2	119	4	US-08-484-537-64	Sequence 64, Appl
30	70	72.2	119	4	US-08-484-537-65	Sequence 65, Appl
31	70	72.2	119	4	US-08-484-537-89	Sequence 89, Appl
32	70	72.2	138	1	US-07-634-278-85	Sequence 85, Appl
33	70	72.2	138	1	US-08-477-728-85	Sequence 85, Appl
34	70	72.2	138	1	US-08-474-040-85	Sequence 85, Appl
35	70	72.2	138	1	US-08-487-200-85	Sequence 85, Appl
36	70	72.2	138	4	US-08-484-537-85	Sequence 85, Appl
37	70	72.2	243	1	US-08-230-843-4	Sequence 4, Appli
38	70	72.2	243	2	US-08-636-936-4	Sequence 4, Appli
39	69	71.1	117	4	US-08-525-539A-76	Sequence 76, Appl
40	69	71.1	117	4	US-08-525-539A-78	Sequence 78, Appl
41	69	71.1	136	4	US-08-525-539A-47	Sequence 47, Appl
42	69	71.1	136	4	US-08-525-539A-63	Sequence 63, Appl
43	68	70.1	273	2	US-08-403-853-18	Sequence 18, Appl
44	67	69.1	115	2	US-08-672-345C-16	Sequence 16, Appl
45	67	69.1	115	4	US-09-214-095D-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-468-252-5
; Sequence 5, Application US/08468252
; Patent No. 5910486
; GENERAL INFORMATION:
; APPLICANT: Curriel, David T.
; APPLICANT: Deshane, Jessy
; APPLICANT: King, C. Richter
; TITLE OF INVENTION: Methods for Modulating Protein Function in
; TITLE OF INVENTION: Cells Using Intracellular Antibody Homologues
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,252
; FILING DATE: 06-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Geary, William C. III
; REGISTRATION NUMBER: 31,359
; REFERENCE/DOCKET NUMBER: UAG-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-252-5

Query Match 76.3%; Score 74; DB 2; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
|:|||||:|||||

DB 171 INPYNGDTYNQKFK 185

```
RESULT 2
US-08-668-706B-5
; Sequence 5, Application US/08668706B
; Patent No. 6028059
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Deshane, Jessy
; APPLICANT: King, C. Richter
; TITLE OF INVENTION: Methods for Modulating Protein Function in
; TITLE OF INVENTION: Cells Using Intracellular Antibody Homologues
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,706B
; FILING DATE: June 24, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Benjamin Aaron
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5874CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; US-08-668-706B-5

Query Match 76.3%; Score 74; DB 3; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00012;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFR 16
Db 171 INPYNGDTNQNQKFK 185

RESULT 3
PCT-US95-10740-5
; Sequence 5, Application PC/TUS9510740
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Deshane, Jessy
; APPLICANT: King, C. Richter
; TITLE OF INVENTION: Methods for Modulating Protein Function in Cells Using Intra
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10740
; FILING DATE: 06-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Geary, William C. III
; REGISTRATION NUMBER: 31,359
; REFERENCE/DOCKET NUMBER: UAG-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-10740-5

Query Match 76.3%; Score 74; DB 5; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00012;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFR 16
Db 171 INPYNGDTNQNQKFK 185

RESULT 4
US-08-137-117D-144
; Sequence 144, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
```

REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-137-117D-144

Query Match 73.2%; Score 71; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.9e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFR 16
Db 2 IDPFNGGTSYNQKFK 16

RESULT 5

US-08-436-717-144
Sequence 144, Application US/08436717
Patent No. 5817790

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436.717
FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137.117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-144

Query Match 73.2%; Score 71; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.9e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFR 16
Db 2 IDPFNGGTSYNQKFK 16

RESULT 6

US-08-888-366-6
Sequence 6, Application US/08888366
Patent No. 5972656

GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888.366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187.407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990.542
FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493.299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324.392
FILING DATE: 14-MAR-1989

ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-366-6

Query Match 73.2%; Score 71; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.00015;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFR 16

Db 45 INPYNGDTSYNQKFK 59
 ; :||||| :|||||

RESULT 7
 US-08-561-521-41
 ; Sequence 41, Application US/08561521
 ; Patent No. 5840299
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; Adhesion Molecule VLA-4
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/561,521
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/186,269A
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15270-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 116 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-561-521-41

Query Match 73.2%; Score 71; DB 2; Length 116;
 Best Local Similarity 80.0%; Pred. No. 0.00017;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFK 16
 ; :||||| :|||||
 Db 51 IDPENGTSYNQKFK 65

RESULT 8
 PCT-US95-01219-41
 ; Sequence 41, Application PC/TUS9501219
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; Adhesion Molecule VLA-4
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/01219
 ; FILING DATE: 25-JAN-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/186,269
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15270-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 116 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-01219-41

Query Match 73.2%; Score 71; DB 5; Length 116;
 Best Local Similarity 80.0%; Pred. No. 0.00017;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFK 16
 ; :||||| :|||||
 Db 51 IDPENGTSYNQKFK 65

RESULT 9
 US-08-137-117D-27
 ; Sequence 27, Application US/08137117D
 ; Patent No. 5795965
 ; GENERAL INFORMATION:
 ; APPLICANT: TSUCHIYA, Masayuki
 ; APPLICANT: SATO, Koh
 ; APPLICANT: BENDIG, Mary
 ; APPLICANT: JONES, Steven
 ; APPLICANT: SALDANHA, Jose
 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 ; INTERLEUKIN-6 RECEPTOR
 ; NUMBER OF SEQUENCES: 158
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/137,117D
 ; FILING DATE: 20-DEC-1993
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP92/00544

;
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-27

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 70 IDPFNGGTSYNQKFK 84

RESULT 10
US-08-137-117D-100
; Sequence 100, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258

;
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-100

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 70 IDPFNGGTSYNQKFK 84

RESULT 11
US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-137-117D-102

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFR 16
Db 70 IDPFGGTSYNQKFK 84

RESULT 12

US-08-137-117D-112
; Sequence 112, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137.117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/RAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-112

Query Match 73.2%; Score 71; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFR 16
Db 70 IDPFGGTSYNQKFK 84

RESULT 13

US-08-436-717-27
; Sequence 27, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436.717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137.117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/RAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-27

Query Match 73.2%; Score 71; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFR 16
Db 70 IDPFGGTSYNQKFK 84

RESULT 14

US-08-436-717-100
; Sequence 100, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-100

Query Match 73.2%; Score 71; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFR 16
Db 70 IDPFNGGTSYNOKFK 84

RESULT 15
US-08-436-717-102
Sequence 102, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-102

Query Match 73.2%; Score 71; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFR 16
Db 70 IDPFNGGTSYNOKFK 84

Search completed: March 10, 2003, 17:02:32
Job time : 16.7069 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 3.93103 Seconds
(without alignments)
29.939 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match	Length	ID	Description
1	21	100.0	6	4	US-09-170-769A-15	Sequence 15, Appl
2	21	100.0	15	4	US-09-026-904-14	Sequence 14, Appl
3	21	100.0	15	6	5248606-25	Patent No. 5248606
4	21	100.0	18	2	US-09-017-205-22	Sequence 22, Appl
5	21	100.0	18	2	US-09-017-205-23	Sequence 23, Appl
6	21	100.0	24	1	US-08-434-198-1	Sequence 1, Appl
7	21	100.0	24	1	US-08-434-198-4	Sequence 4, Appl
8	21	100.0	25	3	US-08-904-448A-12	Sequence 12, Appl
9	21	100.0	26	2	US-08-620-151-13	Sequence 13, Appl
10	21	100.0	30	4	US-09-230-405-11	Sequence 11, Appl
11	21	100.0	40	4	US-08-905-223-387	Sequence 387, App
12	21	100.0	43	2	US-09-097-759-1	Sequence 1, Appl
13	21	100.0	49	1	US-08-178-477B-6	Sequence 6, Appl
14	21	100.0	66	1	US-08-450-360-10	Sequence 10, Appl
15	21	100.0	87	2	US-08-461-990B-20	Sequence 20, Appl
16	21	100.0	92	4	US-09-247-155-98	Sequence 98, Appl
17	21	100.0	109	4	US-09-134-001C-3975	Sequence 3975, Ap
18	21	100.0	113	6	5248606-47	Patent No. 5248606
19	21	100.0	119	1	US-08-300-386A-65	Sequence 65, Appl
20	21	100.0	119	3	US-08-931-645-65	Sequence 65, Appl
21	21	100.0	119	5	PCT-US95-11235-65	Sequence 65, Appl
22	21	100.0	136	3	US-09-187-049-6	Sequence 6, Appl
23	21	100.0	136	4	US-09-222-938A-55	Sequence 55, Appl
24	21	100.0	138	4	US-09-149-476-390	Sequence 390, App
25	21	100.0	140	2	US-08-449-287-4	Sequence 4, Appl
26	21	100.0	146	2	US-08-449-287-10	Sequence 10, Appl
27	21	100.0	146	2	US-08-449-287-12	Sequence 12, Appl

28	21	100.0	149	2	US-08-606-143-24	Sequence 24, Appl
29	21	100.0	150	2	US-08-606-143-26	Sequence 26, Appl
30	21	100.0	150	2	US-08-606-143-29	Sequence 29, Appl
31	21	100.0	151	2	US-08-606-143-19	Sequence 19, Appl
32	21	100.0	152	2	US-08-606-143-4	Sequence 4, Appl
33	21	100.0	152	2	US-08-606-143-5	Sequence 5, Appl
34	21	100.0	152	2	US-08-606-143-6	Sequence 6, Appl
35	21	100.0	152	2	US-08-606-143-7	Sequence 7, Appl
36	21	100.0	152	2	US-08-606-143-9	Sequence 9, Appl
37	21	100.0	152	2	US-08-606-143-10	Sequence 10, Appl
38	21	100.0	152	2	US-08-606-143-12	Sequence 12, Appl
39	21	100.0	152	2	US-08-606-143-13	Sequence 13, Appl
40	21	100.0	152	2	US-08-606-143-15	Sequence 15, Appl
41	21	100.0	152	2	US-08-606-143-16	Sequence 16, Appl
42	21	100.0	152	2	US-08-606-143-18	Sequence 18, Appl
43	21	100.0	152	2	US-08-606-143-20	Sequence 20, Appl
44	21	100.0	152	2	US-08-606-143-21	Sequence 21, Appl
45	21	100.0	152	2	US-08-606-143-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-170-769A-15
; Sequence 15, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACT
; FILE REFERENCE: SCRIPT140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Murine
US-09-170-769A-15

Query Match 100.0%; Score 21; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 1 GLRF 4

RESULT 2
US-09-026-904-14
; Sequence 14, Application US/09026904
; Patent No. 6245502
; GENERAL INFORMATION:
; APPLICANT: Eml, B.
; TITLE OF INVENTION: TARGET SYSTEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026.904
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald J. Flintoft
; REGISTRATION NUMBER: 20,823
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-026-904-14

Query Match 100.0%; Score 21; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
| | | |
Db 1 GLRF 4

RESULT 3

; Patent No. 5248606
; APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,
; ALICE E.R.
; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
; ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
; NUMBER OF SEQUENCES: 49
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/535.636
; FILING DATE: 11-JUN-1990
; SEQ ID NO: 25:
; LENGTH: 15
5248606-25

Query Match 100.0%; Score 21; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
| | | |
Db 8 GLRF 11

RESULT 4

US-09-017-205-22
; Sequence 22, Application US/09017205
; Patent No. 5965357
; GENERAL INFORMATION:
; APPLICANT: Marsden, Howard S
; TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 5965357th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017.205
; FILING DATE: 02-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide from HSV-2 glycoprotein G
; FRAGMENT TYPE: internal
US-09-017-205-22

Query Match 100.0%; Score 21; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
| | | |
Db 15 GLRF 18

RESULT 5

US-09-017-205-23
; Sequence 23, Application US/09017205
; Patent No. 5965357
; GENERAL INFORMATION:
; APPLICANT: Marsden, Howard S
; TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 5965357th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017.205
; FILING DATE: 02-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide from HSV-2 glycoprotein G
; FRAGMENT TYPE: internal
US-09-017-205-23

Query Match 100.0%; Score 21; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
 Db 5 GLRF 8

RESULT 6

US-08-434-198-1
 ; Sequence 1, Application US/08434198
 ; Patent No. 5688911
 ; GENERAL INFORMATION:
 ; APPLICANT: Schneider, et al.
 ; TITLE OF INVENTION: TRK Neurotrophin Binding Motifs
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 ; STREET: 777 Old Saw Mill River Road
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-6707

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434.198
 FILING DATE: 03-MAY-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Kempler PHD., Gail M.
 REGISTRATION NUMBER: 32,143
 REFERENCE/DOCKET NUMBER: REG 400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-7721
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-434-198-1

Query Match 100.0%; Score 21; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
 Db 6 GLRF 9

RESULT 7

US-08-434-198-4
 ; Sequence 4, Application US/08434198
 ; Patent No. 5688911
 ; GENERAL INFORMATION:
 ; APPLICANT: Schneider, et al.
 ; TITLE OF INVENTION: TRK Neurotrophin Binding Motifs
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 ; STREET: 777 Old Saw Mill River Road
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.

ZIP: 10591-6707
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434.198
 FILING DATE: 03-MAY-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kempler PHD., Gail M.
 REGISTRATION NUMBER: 32,143
 REFERENCE/DOCKET NUMBER: REG 400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-7721
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-434-198-4

Query Match 100.0%; Score 21; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
 Db 6 GLRF 9

RESULT 8

US-08-904-446A-12
 ; Sequence 12, Application US/08904446A
 ; Patent No. 6029114
 ; GENERAL INFORMATION:
 ; APPLICANT: Shamovsky, Igor L.
 ; APPLICANT: Ross, Gregory M.
 ; APPLICANT: Riopelle, Richard J.
 ; APPLICANT: Weaver, Donald F.
 ; TITLE OF INVENTION: Molecular Modelling of Neurotrophin-Receptor
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dowell & Dowell, P.C.
 ; STREET: 1215 Jefferson Davis Highway, Suite 309
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: United States of America
 ; ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/904.446A
 FILING DATE: 31-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9616105.4
 FILING DATE: 31-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: RALPH A. DOWELL
 REGISTRATION NUMBER: 26868
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 415-2555
 TELEFAX: (703) 415-2559
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:

;
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..25
; OTHER INFORMATION: /note= "Second leucine rich motif"
; OTHER INFORMATION:
US-08-904-446A-12

Query Match 100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 10 GLRF 13

RESULT 9
US-08-620-151-13
; Sequence 13, Application US/08620151
; Patent No. 5928955
; GENERAL INFORMATION:
; APPLICANT: Imperiali, Barbara
; APPLICANT: Walkup, Grant K.
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
; TITLE OF INVENTION: DIVALENT ZINC
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; STREET: Plaza Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60611-5599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,151
; FILING DATE: 22-MAR-1996
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: Shannon, Karen L.
; REGISTRATION NUMBER: 36,675
; REFERENCE/DOCKET NUMBER: 8597/6
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-620-151-13

Query Match 100.0%; Score 21; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 8 GLRF 11

RESULT 10
US-09-230-405-11
; Sequence 11, Application US/09230405
; Patent No. 6337074
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-VIRAL AGENT
; FILE REFERENCE: P17970C
; CURRENT APPLICATION NUMBER: US/09/230,405
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide derived
; OTHER INFORMATION: from herpes simplex virus
US-09-230-405-11

Query Match 100.0%; Score 21; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 22 GLRF 25

RESULT 11
US-08-905-223-387
; Sequence 387, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 387:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:

NAME/KEY: sig_peptide
 LOCATION: -36...-1
 IDENTIFICATION METHOD: Von Heijne matrix
 OTHER INFORMATION: score 3.8
 OTHER INFORMATION: seq GTDSLFLPPCP/CP
 US-08-905-223-387

Query Match 100.0%; Score 21; DB 4; Length 40;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
 Db 6 GLRF 9

RESULT 12

US-09-097-759-1
 Sequence 1, Application US/09097759A
 Patent No. 5972663

GENERAL INFORMATION:

APPLICANT: Winterhalter Mr., Christopher
 APPLICANT: Leinfelder Mr., Walfred
 TITLE OF INVENTION: Microorganisms and Processes for the Fermentative
 TITLE OF INVENTION: Preparation of L-cysteine,
 TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives
 FILE REFERENCE: Winterhalter
 CURRENT APPLICATION NUMBER: US/09/097,759A
 CURRENT FILING DATE: 1998-06-16
 EARLIER APPLICATION NUMBER: DE 197 26 083
 EARLIER FILING DATE: 1997-06-19
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
 LENGTH: 43

TYPE: PRT
 ORGANISM: Escherichia coli
 US-09-097-759-1

Query Match 100.0%; Score 21; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
 Db 37 GLRF 40

RESULT 13

US-08-178-477B-6
 Sequence 6, Application US/08178477B
 Patent No. 5756343

GENERAL INFORMATION:

APPLICANT: WU, CARL; CLOS, JOACHIM;
 APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN, SRIDHAR
 TITLE OF INVENTION: CELL STRESS
 TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
 NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/178,477B
 FILING DATE: 07-JAN-1994

CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/617,910
 FILING DATE: 26-NOV-1990
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: CAROL M. GRUPPI
 REGISTRATION NUMBER: 37,341
 REFERENCE/DOCKET NUMBER: 2026-4103US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 49
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-178-477B-6

Query Match 100.0%; Score 21; DB 1; Length 49;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
 Db 25 GLRF 28

RESULT 14

US-08-450-360-10
 Sequence 10, Application US/08450360
 Patent No. 5656457

GENERAL INFORMATION:

APPLICANT: Parkes, Deborah Lynn
 APPLICANT: Coates, Stephen Ralph
 TITLE OF INVENTION: Herpes Simplex Virus Type 2-Glycoprotein G
 TITLE OF INVENTION: Proteins and Polypeptides
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder
 STREET: 6 Mariposa Court
 CITY: Tiburon
 STATE: California
 COUNTRY: USA
 ZIP: 94920

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,360
 FILING DATE: 25-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/129,021
 FILING DATE: 29-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Lauder, Leona L.
 REGISTRATION NUMBER: 30,863
 REFERENCE/DOCKET NUMBER: D-0012.2A
 TELEPHONE: 415-435-2034
 TELEFAX: 415-435-0727

GENERAL INFORMATION:

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 66 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-450-360-10

Query Match 100.0%; Score 21; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
Db 48 GLRF 51

RESULT 15

US-08-461-990B-20
; Sequence 20, Application US/08461990B
; Patent No. 5851810
; GENERAL INFORMATION:
; APPLICANT: JOHN S. BLANCHARD
; TITLE OF INVENTION: NUCLEIC ACID ENCODING RHODOCOCCUS
; TITLE OF INVENTION: PHENYLALANINE DEHYDROGENASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,990B
; FILING DATE: JUNE 5, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG J. ARNOLD
; REGISTRATION NUMBER: 34,287
; REFERENCE/DOCKET NUMBER: 96700/370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PROTEIN
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: C. SYMBIOSUM
; INDIVIDUAL ISOLATE: GLUTAMATE DEHYDROGENASE
US-08-461-990B-20

Query Match 100.0%; Score 21; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
|
|
|
Db 13 GLRF 16

Search completed: March 10, 2003, 17:02:33
Job time : 4.93103 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 8.10345 Seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	58	100.0	10	10	US-09-924-099-6
2	58	100.0	113	10	US-09-924-099-2
3	58	100.0	237	10	US-09-924-099-9
4	58	100.0	243	10	US-09-924-099-10
5	48	82.8	117	9	US-09-923-854-4
6	48	82.8	142	10	US-09-772-120-8
7	47	81.0	123	10	US-09-217-268B-28
8	47	81.0	123	10	US-09-217-268B-36
9	44	75.9	98	9	US-10-194-975-11
10	42	72.4	111	9	US-10-032-482-5
11	42	72.4	125	9	US-09-929-665-20
12	42	72.4	125	9	US-09-929-546-20
13	42	72.4	249	1	US-08-779-457-48
14	41	70.7	98	10	US-09-840-459-41
15	41	70.7	118	9	US-09-144-886-63
16	41	70.7	132	9	US-09-982-107-14
17	41	70.7	669	9	US-09-807-721-2
18	40	69.0	98	9	US-10-194-975-45
19	40	69.0	98	10	US-09-850-165-89

20 40 69.0 98 12 US-10-025-687-16 Sequence 16, Appli
21 40 69.0 120 12 US-10-025-687-6 Sequence 6, Appli
22 40 69.0 135 9 US-09-249-011A-2 Sequence 2, Appli
23 40 69.0 135 9 US-09-249-011A-6 Sequence 6, Appli
24 40 69.0 235 10 US-09-888-721-34 Sequence 34, Appli
25 40 69.0 262 9 US-09-956-086-4 Sequence 4, Appli
26 40 69.0 262 9 US-09-956-087-4 Sequence 4, Appli
27 40 69.0 269 10 US-09-888-721-36 Sequence 36, Appli
28 40 69.0 282 9 US-09-985-442-7 Sequence 7, Appli
29 40 69.0 282 10 US-09-888-721-38 Sequence 38, Appli
30 40 69.0 282 10 US-09-983-580-7 Sequence 7, Appli
31 40 69.0 287 10 US-09-888-721-40 Sequence 40, Appli
32 40 69.0 291 10 US-09-888-721-44 Sequence 44, Appli
33 40 69.0 296 10 US-09-888-721-42 Sequence 42, Appli
34 40 69.0 461 9 US-09-249-011A-24 Sequence 24, Appli
35 40 69.0 672 9 US-09-900-766-1 Sequence 1, Appli
36 39 67.2 118 10 US-09-905-243-70 Sequence 70, Appli
37 39 67.2 119 10 US-09-850-165-54 Sequence 54, Appli
38 39 67.2 128 10 US-09-850-165-52 Sequence 52, Appli
39 39 67.2 239 10 US-09-808-037-6 Sequence 6, Appli
40 38 65.5 96 10 US-09-905-243-15 Sequence 15, Appli
41 38 65.5 98 9 US-10-194-975-7 Sequence 7, Appli
42 38 65.5 100 10 US-09-840-459-37 Sequence 37, Appli
43 38 65.5 101 10 US-09-840-459-42 Sequence 42, Appli
44 38 65.5 101 10 US-09-840-459-46 Sequence 46, Appli
45 38 65.5 106 9 US-10-032-482-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-924-099-6
; Sequence 6, Application US/09924099

; Patent NO. US20020128450A1

; GENERAL INFORMATION:

; APPLICANT: NISHIDA, Yoshihiro

; APPLICANT: OKURA, Takanori

; APPLICANT: TANIMOTO, Tadao

; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: PEPTIDE

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/924,099

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22

; NUMBER OF SEQ ID NOS: 33

; SEQ ID NO 6

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-924-099-6

Query Match 100.0%; Score 58; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSTDYFIY 10

Db 1 GYSTDYFIY 10

RESULT 2

US-09-924-099-2

; Sequence 2, Application US/09924099

; Patent No. US20020128450A1

; GENERAL INFORMATION:

; APPLICANT: NISHIDA, Yoshihiro

; APPLICANT: OKURA, Takanori

```
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-2

Query Match      100.0%; Score 58; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
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Db       26 GYSFTDYFIY 35

RESULT 3
US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match      100.0%; Score 58; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
        |||||
Db       26 GYSFTDYFIY 35

RESULT 4
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
```

```
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match      100.0%; Score 58; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTDYFIY 10
        |||||
Db       26 GYSFTDYFIY 35

RESULT 5
US-09-293-854-4
; Sequence 4, Application US/09293854
; Patent No. US20020168357A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; APPLICANT: Jiao, Jin-an
; APPLICANT: Esperanza, Nieves
; APPLICANT: Lawrence, Lupechen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,854
; FILING DATE: 16-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/814,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
```


SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4

Query Match 82.8%; Score 48; DB 9; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db 26 GYSFTDNYV 35

RESULT 6

US-09-772-120-8
; Sequence 8, Application US/09772120
; Patent No. US20010014328A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; Graziano, Robert
; Keiser, Tibor

TITLE OF INVENTION: Therapeutic Multispecific Compounds
Comprised of Anti-Fc
{SYMBOL 97 \f "Symbol"} Receptor Antibodies

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772,120

FILING DATE: 26-Jan-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,011

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: MXI-064CP

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 142 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-772-120-8

Query Match 82.8%; Score 48; DB 10; Length 142;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10

Db 45 GYSFTDYIF 54

RESULT 7

US-09-217-268B-28
; Sequence 28, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M

TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Ep

FILE REFERENCE: 2720.IUS

CURRENT APPLICATION NUMBER: US/09/217,268B

CURRENT FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patent In version 3.1

SEQ ID NO 28

LENGTH: 123

TYPE: PRT

ORGANISM: Murine R3 antibody

FEATURE:

NAME/KEY: MISC_FEATURE

OTHER INFORMATION: Deduced amino acid sequence of VH of murine R3 antibody

US-09-217-268B-28

Query Match 81.0%; Score 47; DB 10; Length 123;

Best Local Similarity 70.0%; Pred. No. 0.56;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10

Db 26 GYFTNYVIY 35

RESULT 8

US-09-217-268B-36
; Sequence 36, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M

TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Ep

FILE REFERENCE: 2720.IUS

CURRENT APPLICATION NUMBER: US/09/217,268B

CURRENT FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patent In version 3.1

SEQ ID NO 36

LENGTH: 123

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Amino acid sequence of humanized VH of murine R3 antibody cont

US-09-217-268B-36

Query Match 81.0%; Score 47; DB 10; Length 123;

Best Local Similarity 70.0%; Pred. No. 0.56;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10

Db 26 GYFTNYVIY 35

RESULT 9

US-10-194-975-11

; Sequence 11, Application US/10194975

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; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-11

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Query Match          75.9%; Score 44; DB 9; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GYSFTDYFI 10
Db 26 GYTFTDYIM 35

```

RESULT 10

```

US-10-032-482-5
; Sequence 5, Application US/10032482
; Publication No. US20020197270A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/10/032,482
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US/09/445,602
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-032-482-5

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Query Match          72.4%; Score 42; DB 9; Length 111;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 GYSFTDYFI 9
Db 23 GYTFTDYIM 31

```

RESULT 11

```

US-09-929-665-20
; Sequence 20, Application US/09929665
; Publication No. US2003003101A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024

```

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; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-20

```

```

Query Match          72.4%; Score 42; DB 9; Length 125;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GYSFTDYFI 9
Db 26 GYTFTDYIM 34

```

RESULT 12

```

US-09-929-546-20
; Sequence 20, Application US/09929546
; Publication No. US20030031673A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-20

```

```

Query Match          72.4%; Score 42; DB 9; Length 125;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GYSFTDYFI 9
Db 26 GYTFTDYIM 34

```

RESULT 13

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US-08-779-457-48
; Sequence 48, Application US/08779457
; Publication No. US20020193571A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: RODRIGUES, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

```

; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-779-457-48

Query Match 72.4%; Score 42; DB 1; Length 249;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
|:|:|:|:|:
Db 26 GYFTGYMY 35

RESULT 14

US-09-840-459-41
; Sequence 41, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 05/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-840-459-41

Query Match 70.7%; Score 41; DB 10; Length 98;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
|:|:|:|:|:
Db 26 GYFTSDYYMY 35

RESULT 15

US-09-144-886-63
; Sequence 63, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 63
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: C25 region VH epitope 2
; US-09-144-886-63

Query Match 70.7%; Score 41; DB 9; Length 118;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
|:|:|:|:|:
Db 26 GYFTSDYYMY 35

Search completed: March 10, 2003, 17:11:29
Job time : 9.10345 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	97	100.0	17	10	US-09-924-099-7		Sequence 7, Appli
2	97	100.0	113	10	US-09-924-099-2		Sequence 2, Appli
3	97	100.0	237	10	US-09-924-099-9		Sequence 9, Appli
4	97	100.0	0	243	US-09-924-099-10		Sequence 10, Appli
5	69	71.1	117	9	US-09-936-206A-76		Sequence 76, Appli
6	69	71.1	117	9	US-09-936-206A-78		Sequence 78, Appli
7	69	71.1	136	9	US-09-936-206A-47		Sequence 47, Appli
8	69	71.1	136	9	US-09-936-206A-63		Sequence 63, Appli
9	68	70.1	117	9	US-09-982-992A-6		Sequence 6, Appli
10	66	68.0	117	9	US-09-736-258-48		Sequence 48, Appli
11	66	68.0	117	9	US-09-736-258-49		Sequence 49, Appli
12	66	68.0	125	9	US-09-929-665-20		Sequence 20, Appli
13	66	68.0	125	9	US-09-929-546-20		Sequence 20, Appli
14	66	68.0	135	9	US-09-736-258-37		Sequence 37, Appli
15	66	68.0	253	9	US-09-736-258-44		Sequence 44, Appli
16	66	68.0	253	9	US-09-736-258-52		Sequence 52, Appli
17	66	68.0	253	9	US-09-736-258-55		Sequence 55, Appli
18	66	68.0	256	9	US-09-736-258-70		Sequence 70, Appli
19	66	68.0	298	9	US-09-736-258-60		Sequence 60, Appli

```
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-2

Query Match 100.0%; Score 97; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy * 1 DIDPYNGDTSYNQKFRD 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 DIDPYNGDTSYNQKFRD 66

RESULT 3
US-09-924-099-9
; Sequence 9, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-9

Query Match 100.0%; Score 97; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFRD 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 DIDPYNGDTSYNQKFRD 66

RESULT 4
US-09-924-099-10
; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
```

```
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced peptide in the form of a single
; OTHER INFORMATION: chain
; OTHER INFORMATION: variable region fragment (scFv) which neutralizes IL-18
US-09-924-099-10

Query Match 100.0%; Score 97; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFRD 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 DIDPYNGDTSYNQKFRD 66

RESULT 5
US-09-956-206A-76
; Sequence 76, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERTANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
```

REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-956-206A-76

Query Match 71.1%; Score 69; DB 9; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00054;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFRD 17
|:||||| | |||||:|
Db 51 INPYNGTVYNOKFQD 66

RESULT 6

US-09-956-206A-78
; Sequence 78, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956.206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WITT, ERIC

REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-956-206A-78

Query Match 71.1%; Score 69; DB 9; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00054;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFRD 17
|:||||| | |||||:|
Db 51 INPYNGTVYNOKFQD 66

RESULT 7

US-09-956-206A-47
; Sequence 47, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956.206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WITT, ERIC

REGISTRATION NUMBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-956-206A-47

Query Match 71.1%; Score 69; DB 9; Length 136;
Best Local Similarity 75.0%; Pred. No. 0.00063;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFRD 17
|:||||| | |||||:|

Db 70 INPYNGTGVNQKFD 85

RESULT 8

US-09-956-206A-63

Sequence 63, Application US/09956206A

Patent No. US20020164339A1

GENERAL INFORMATION:

APPLICANT: DO COUTO, FERNANDO J.R.

CERIANI, ROBERTO L.

PETERSON, JERRY A.

TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND

METHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956.206A

FILING DATE: 19-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/525,539

FILING DATE: 14-SEP-1995

APPLICATION NUMBER: PCT/US95/11683

FILING DATE: 14-SEP-1995

APPLICATION NUMBER: 08/487,598

FILING DATE: 7-JUNE-1995

APPLICATION NUMBER: 08/307,868

FILING DATE: 16-SEPT-1994

ATTORNEY/AGENT INFORMATION:

NAME: WITT, ERIC

REGISTRATION NUMBER: 44,408

REFERENCE/DOCKET NUMBER: 276332000101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 136 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 63:

US-09-956-206A-63

Query Match 71.1%; Score 69; DB 9; Length 136;

Best Local Similarity 75.0%; Pred. No. 0.00063;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGTGVNQKFD 17

Db 70 INPYNGTGVNQKFD 85

RESULT 9

US-09-982-992A-6

Sequence 6, Application US/09982992A

Patent No. US20020164337A1

GENERAL INFORMATION:

APPLICANT: PATTI, Joseph M. et al.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE MAP PROTEIN AND METHOD OF USE IN TRB

TITLE OF INVENTION: AND PREVENTING INFECTIONS

FILE REFERENCE: P06922US02/BAS

CURRENT APPLICATION NUMBER: US/09/982,992A

CURRENT FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/277,287

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/241,832

PRIOR FILING DATE: 2000-10-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.0

SEQ ID NO. 6

LENGTH: 117

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-982-992A-6

Query Match 70.1%; Score 68; DB 9; Length 117;

Best Local Similarity 68.8%; Pred. No. 0.00078;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGTGVNQKFD 17

Db 51 IDPYDSETHYNQKFD 66

RESULT 10

US-09-726-258-48

Sequence 48, Application US/09726258

Publication No. US20030021790A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsui, Vanessa

APPLICANT: Koumenis, Iphigenia

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

APPLICANT: Shahrokhi, Zahra

APPLICANT: Zapata, Gerardo A.

TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND

TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/726,258

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/234,182

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/094003

FILING DATE: 24-JUL-1998

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R4-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear


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; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-726-258-37
Query Match 68.0%; Score 66; DB 9; Length 135;
Best Local Similarity 73.3%; Pred. No. 0.0019;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 51 IDPSNGETTYNQKFK 65

RESULT 15
US-09-726-258-44
; Sequence 44, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
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; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-726-258-44
Query Match 68.0%; Score 66; DB 9; Length 253;
Best Local Similarity 73.3%; Pred. No. 0.0036;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
Db 74 IDPSNGETTYNQKFK 88

Search completed: March 10, 2003, 17:11:29
Job time : 13.7759 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:57:06 ; Search time 3.24138 seconds
(without alignments)
52.040 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	10	US-09-924-099-8
2	21	100.0	7	9	US-09-968-561A-99
3	21	100.0	7	10	US-09-192-854-61
4	21	100.0	21	9	US-09-974-879-281
5	21	100.0	24	9	US-10-164-359-11
6	21	100.0	39	10	US-09-864-761-34201
7	21	100.0	45	10	US-09-864-761-44502
8	21	100.0	51	10	US-09-864-761-34507
9	21	100.0	53	10	US-09-764-877-1721
10	21	100.0	54	10	US-09-864-761-42767
11	21	100.0	57	10	US-09-764-877-1214
12	21	100.0	59	10	US-09-864-761-46881
13	21	100.0	65	10	US-09-867-550-1842
14	21	100.0	80	10	US-09-862-179A-26
15	21	100.0	84	10	US-09-864-761-47725
16	21	100.0	87	10	US-09-764-880-427
17	21	100.0	89	9	US-10-078-770-104
18	21	100.0	89	9	US-10-078-770-112
19	21	100.0	89	10	US-09-764-853-466

20	21	100.0	100	9	US-09-974-879-279	Sequence 279, App
21	21	100.0	101	10	US-09-864-761-37100	Sequence 37100, A
22	21	100.0	106	10	US-09-925-297-790	Sequence 790, App
23	21	100.0	107	10	US-09-734-017A-36	Sequence 36, Appl
24	21	100.0	110	9	US-09-969-763-10	Sequence 10, Appl
25	21	100.0	113	10	US-09-924-099-2	Sequence 2, Appl
26	21	100.0	116	10	US-09-867-550-146	Sequence 146, App
27	21	100.0	117	9	US-09-906-209-6	Sequence 6, Appl
28	21	100.0	121	10	US-09-864-761-46883	Sequence 46883, A
29	21	100.0	125	10	US-09-764-898-245	Sequence 245, App
30	21	100.0	127	10	US-09-815-242-10432	Sequence 10432, A
31	21	100.0	128	10	US-09-764-870-277	Sequence 277, App
32	21	100.0	139	10	US-09-864-761-40558	Sequence 40558, A
33	21	100.0	143	9	US-09-925-299-1142	Sequence 1142, Ap
34	21	100.0	143	10	US-09-925-299-1142	Sequence 1142, Ap
35	21	100.0	148	10	US-09-908-711-91	Sequence 91, Appl
36	21	100.0	154	10	US-09-925-301-851	Sequence 851, App
37	21	100.0	156	10	US-09-870-756-6	Sequence 6, Appl
38	21	100.0	156	10	US-09-874-585B-6	Sequence 6, Appl
39	21	100.0	159	10	US-09-925-297-727	Sequence 727, App
40	21	100.0	167	9	US-09-738-626-4384	Sequence 4384, Ap
41	21	100.0	170	9	US-09-975-719-158	Sequence 158, App
42	21	100.0	176	12	US-10-062-234-230	Sequence 230, App
43	21	100.0	179	10	US-09-970-711-44	Sequence 44, Appl
44	21	100.0	180	10	US-09-864-761-37144	Sequence 37144, A
45	21	100.0	186	10	US-09-925-301-1414	Sequence 1414, Ap

ALIGNMENTS

RESULT 1
US-09-924-099-8
; Sequence 8, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-924-099-8

Query Match 100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 1 GLRF 4

RESULT 2
US-09-968-561A-99
; Sequence 99, Application US/09968561A
; Patent No. US2002016462A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory

; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-99

Query Match 100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 2 GLRF 5

RESULT 3

US-09-192-854-61
; Sequence 61, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:

; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-61

Query Match 100.0%; Score 21; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 2 GLRF 5

RESULT 4

US-09-974-879-281
; Sequence 281, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
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; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
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; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-281

Query Match 100.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 18 GLRF 21

RESULT 5

US-10-164-359-11
; Sequence 11, Application US/10164359
; Publication No. US20030012776A1
; GENERAL INFORMATION:
; APPLICANT: Chin, Khew-Voon
; TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement
; TITLE OF INVENTION: Stress
; FILE REFERENCE: 601-1-108US
; CURRENT APPLICATION NUMBER: US/10/164,359
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: PCT/US00/33438
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,418
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-359-11

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Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
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Db 5 GLRF 8

RESULT 6
US-09-864-761-34201
; Sequence 34201, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.3e+02
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

Query Match      100.0%; Score 21; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
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Db 25 GLRF 28

RESULT 7
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; Sequence 44502, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44502
; LENGTH: 45
; TYPE: PRT
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86
; OTHER INFORMATION: SWISSPROT HIT: Q09890, EVALUE 4.80e+00
US-09-864-761-44502

Query Match          100.0%; Score 21; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 13 GLRF 16

RESULT 8
US-09-864-761-34507
; Sequence 34507, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
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; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34507
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006365.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
US-09-864-761-34507
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Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GLRF 4
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Db 42 GLRF 45
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RESULT 9
US-09-764-877-1721
; Sequence 1721, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1721
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (41)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1721
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Query Match          100.0%; Score 21; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GLRF 4
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Db 35 GLRF 38
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RESULT 10
US-09-864-761-42767
; Sequence 42767, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
```

APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 42767
LENGTH: 54
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035587.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3
OTHER INFORMATION: SWISSPROT HIT: P17937, EVALUE 4.00e-04
OTHER INFORMATION: EST_HUMAN HIT: BE409626.1, EVALUE 7.00e-25
US-09-864-761-42767

Query Match 100.0%; Score 21; DB 10; Length 54;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
| | | |
Db 6 GLRF 9

RESULT 11
US-09-764-877-1214
Sequence 1214, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1214
LENGTH: 57
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (12)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (13)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1214

Query Match 100.0%; Score 21; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
| | | |
Db 32 GLRF 35

RESULT 12

US-09-864-761-46881
Sequence 46881, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46881
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000494.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EST_HUMAN HIT: AW270799.1, EVALUE 3.00e-04
; OTHER INFORMATION: SWISSPROT HIT: P12690, EVALUE 2.00e+00
US-09-864-761-46881
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Best Local Similarity 100.0%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GLRF 4
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Db 17 GLRF 20
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RESULT 13

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; Sequence 1842, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1842
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1842
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Best Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GLRF 4
    ||||
Db 25 GLRF 28
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RESULT 14

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US-09-862-179A-26
; Sequence 26, Application US/09862179A
; Patent No. US20020147306A1
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; GENERAL INFORMATION:
; APPLICANT: Lin, Danny
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
; FILE REFERENCE: MTSI-PO1-009
; CURRENT APPLICATION NUMBER: US/09/862,179A
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-179A-26
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Best Local Similarity 100.0%; Pred. No. 11e+02;
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Qy 1 GLRF 4
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Db 39 GLRF 42
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RESULT 15

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US-09-864-761-47725
; Sequence 47725, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
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; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47725
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL033520.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EST_HUMAN HIT: BE897334.1, EVALUATE 3.00e-10
US-09-864-761-47725

Query Match 100.0%; Score 21; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
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Db 16 GLRF 19

Search completed: March 10, 2003, 17:11:29
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 28.2759 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	21	Mouse anti-IL-18 a
2	58	100.0	113	21	Mouse anti-IL-18 a
3	58	100.0	137	21	Mouse heavy chain
4	58	100.0	237	21	EscFv#125-2H recom
5	58	100.0	243	21	EscFv#125-2H, HT re
6	53	91.4	242	23	Human BlyS binding
7	53	91.4	242	23	Human BlyS binding
8	50	86.2	120	22	Anti-PF4/heparin c
9	50	86.2	253	23	Human BlyS binding
10	49	84.5	112	23	Human mAb 12B1 hea

11	84.5	114	23	AAG80197	Human gp96 Ab clon
12	82.8	117	19	AAW71288	Human anti-tissue
13	82.8	142	19	AAW48249	A77 anti-Fc alpha
14	82.8	142	22	AAE08555	Murine A77 anti-Fc
15	82.8	142	22	AAW74622	A77 anti-Fc-alpha-
16	82.8	353	20	AAW06273	Anti Fc alpha rece
17	81.0	97	22	ABP01374	Human OREP protein
18	81.0	122	22	ABG02111	Human autoantibody
19	81.0	123	17	AAW92992	Humanised antibody
20	81.0	123	17	AAW92990	Monoclonal antibody
21	81.0	249	23	ABP45719	Human BlyS binding
22	79.3	110	19	AAW39881	Heavy chain of the
23	79.3	116	19	AAW39889	Heavy chain of the
24	79.3	118	20	AAW52755	Anti-tissue factor
25	79.3	118	20	AAW52756	Anti-tissue factor
26	79.3	215	21	AAW78254	Mouse agglutinin
27	79.3	245	23	ABP45889	Human BlyS binding
28	77.6	115	19	AAW39814	Variable domain of
29	77.6	116	17	AAW03742	Murine monoclonal
30	77.6	117	23	AAW99848	Mouse AC10 antibod
31	77.6	118	20	AAW52760	Anti-tissue factor
32	77.6	118	20	AAW30188	Amino acid sequenc
33	77.6	122	22	ABW62868	Anti-SAF-1 monoclo
34	77.6	137	19	AAW79226	Humanised LO-CD2a
35	77.6	137	19	AAW56350	Humanised LO-CD2a
36	77.6	137	20	AAW30189	Amino acid sequenc
37	77.6	138	21	AAW56873	MAB CT-M-01 heavy
38	77.6	139	14	AAW33950	CTM01 VH. Synthet
39	77.6	139	14	AAW33953	gh1 variable domai
40	77.6	139	18	AAW29750	Anti-HMFG MAB CTMO
41	77.6	139	18	AAW29753	CDR-grafted human
42	77.6	139	21	AAW56877	gh1 variable domai
43	77.6	251	23	ABW45325	Human BlyS binding
44	77.6	252	23	ABW45943	Human BlyS binding
45	77.6	255	23	ABW45396	Human BlyS binding

ALIGNMENTS

RESULT 1
AAW44592
ID AAY44592 standard; Protein; 10 AA.
XX
AC AAY44592;
XX
DT 04-APR-2000 (first entry)
XX

Mouse anti-IL-18 antibody VH complementarity-determining region-1.
DE
XX
XX
XX
KW Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;
KW complementarity-determining region; CDR; hybridoma #125-2H; mouse;
KW monoclonal antibody #125-2HmAb; Interleukin-18; antiinflammatory;
KW immunosuppressive; leucocytopenic; antiangiogenic; antipruritic;
KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
KW inflammatory disorder; immunoreaction;
XX
OS Mus musculus.
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX

Query Match 100.0%; Score 58; DB 21; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTDYFIY 10
| | | | | | | | | |
Db 45 GYSFTDYFIY 54

RESULT 4
AAY44595
ID AAY44595 standard; Protein; 237 AA.

XX AC AAY44595;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H recombinant protein.

XX KW EscFv#125-2H recombinant protein; interleukin-18; mouse;
XX KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
XX KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
XX KW antialgic; antipyretic.

XX OS Mus musculus.
XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"

XX EP974600-A2.

XX PD 26-JAN-2000.

XX PF 24-JUN-1999; 99EP-0304977.

XX PR 24-JUN-1998; 98JP-0177580.

XX PR 12-OCT-1998; 98JP-0289044.

XX PR 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

XX N-PSDB; AAZ49542.

XX PT New artificially produced peptide for neutralizing biological activity
XX PT of interleukin-18, useful for treating and preventing immunopathies,
XX PT inflammatory disorders and autoimmune diseases -

XX PS Claim 8; Page 19-20; 32pp; English.

XX CC The present sequence is EscFv#125-2H protein encoded by recombinant cDNA
XX CC pEscFv#125-2H for neutralizing interleukin-18. The protein is produced
XX CC from hybridoma #125-2H by transforming pEscFv#125-2H in competent
XX CC E. coli cells. This is useful for treating and preventing immunopathies,
XX CC inflammatory disorders and autoimmune diseases which are caused by
XX CC excessive immunoreaction. The protein has anti-allergic,
XX CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,
XX CC antialgic, antipyretic and hepatic-function improving activities.

XX SQ Sequence 237 AA;

Query Match 100.0%; Score 58; DB 21; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTDYFIY 10
| | | | | | | | | |
Db 26 GYSFTDYFIY 35

RESULT 5
AAY44596
ID AAY44596 standard; Protein; 243 AA.

XX AC AAY44596;

XX DT 04-APR-2000 (first entry)

XX DE EscFv#125-2H.HT recombinant protein.

XX KW EscFv#125-2H.HT recombinant protein; interleukin-18; mouse;
XX KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
XX KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
XX KW antialgic; antipyretic.

XX OS Mus musculus.
XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 1..113
FT /note= "Heavy chain variable region"
FT Domain 114..130
FT /note= "Glycine-serine linker"
FT Domain 131..237
FT /note= "Light chain variable region"

XX EP974600-A2.

XX PD 26-JAN-2000.

XX PF 24-JUN-1999; 99EP-0304977.

XX PR 24-JUN-1998; 98JP-0177580.

XX PR 12-OCT-1998; 98JP-0289044.

XX PR 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

XX N-PSDB; AAZ49543.

XX PT New artificially produced peptide for neutralizing biological activity
XX PT of interleukin-18, useful for treating and preventing immunopathies,
XX PT inflammatory disorders and autoimmune diseases -

XX PS Claim 8; Page 20-21; 32pp; English.

XX CC The present sequence is EscFv#125-2H.HT protein encoded by
XX CC recombinant cDNA pEscFv#125-2H.HT for neutralising interleukin-18. The
XX CC protein is produced from hybridoma #125-2H by transforming
XX CC pEscFv#125-2H.HT in competent E. coli cells. There are six histidine
XX CC residues positioned after the light chain variable region. This protein
XX CC is useful for treating and preventing immunopathies, inflammatory
XX CC disorders and autoimmune diseases which are caused by excessive
XX CC immunoreaction. The protein has anti-allergic, anti-inflammatory,
XX CC immunosuppressive, hematopoietic, leukocytopoietic, antialgic,
XX CC antipyretic and hepatic-function improving activities.

XX SQ Sequence 243 AA;

Query Match 100.0%; Score 58; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTDYFIY 10

Db 26 GYSFTDYFIH 35
|||||
RESULT 6
ABP45974
ID ABP45974 standard; Protein: 242 AA.
XX AC
XX ABP45974;
XX DT 19-AUG-2002 (first entry)
XX DE Human BLYS binding scFv SEQ ID 1985.
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN W0200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US19110.
XX PR 16-JUN-2000; 2000US-212210P.
XX PR 17-OCT-2000; 2000US-240816P.
XX PR 16-MAR-2001; 2001US-276248P.
XX PR 21-MAR-2001; 2001US-277379P.
XX PR 25-MAY-2001; 2001US-293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR
XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX PS
XX PS Claim 1; Page 2769-2770; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
CC and so may be used to detect and quantitate the presence of BLYS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLYS. They may also be
CC administered to treat diseases associated with aberrant BLYS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP45974-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX SQ Sequence 242 AA;
Query Match 91.4%; Score 53; DB 23; Length 242;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTDYFIH 10
|||||
Db 26 GYSFTDYFIH 35

Db 26 GYSFTDYFIH 35
RESULT 7
ABP46088
ID ABP46088 standard; Protein: 242 AA.
XX AC
XX ABP46088;
XX DT 19-AUG-2002 (first entry)
XX DE Human BLYS binding scFv SEQ ID 2099.
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN W0200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US19110.
XX PR 16-JUN-2000; 2000US-212210P.
XX PR 17-OCT-2000; 2000US-240816P.
XX PR 16-MAR-2001; 2001US-276248P.
XX PR 21-MAR-2001; 2001US-277379P.
XX PR 25-MAY-2001; 2001US-293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR
XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX PS
XX PS Claim 1; Page 2901-2902; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
CC and so may be used to detect and quantitate the presence of BLYS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLYS. They may also be
CC administered to treat diseases associated with aberrant BLYS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX SQ Sequence 242 AA;
Query Match 91.4%; Score 53; DB 23; Length 242;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTDYFIH 10
|||||
Db 26 GYSFTDYFIH 35

immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.

WO200202641-A1.

10-JAN-2002.

15-JUN-2001; 2001WO-US19110.

16-JUN-2000; 2000US-212210P.

17-OCT-2000; 2000US-240816P.

16-MAR-2001; 2001US-276248P.

21-MAR-2001; 2001US-277379P.

25-MAY-2001; 2001US-293499P.

(HUMA-) HUMAN GENOME SCI INC.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

WPI; 2002-114799/15.

Antibodies against B Lymphocyte Stimulating polypeptides, useful for

the diagnosis and treatment of cancers and immune disorders -

Claim 1; Page 2224-2225; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to
 B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 tumour necrosis factor (TNF) super family and induces B cell
 proliferation and differentiation. The antibodies of the invention have
 cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 antirheumatic and antiAIDS activity and can be used in vaccines to
 inhibit the expression and activity of Blys. The antibodies bind to Blys
 and so may be used to detect and quantitate the presence of Blys in
 biological samples and may be used in this way to diagnose disease
 associated with aberrant expression of Blys. They may also be
 administered to treat diseases associated with aberrant Blys expression
 and activity such as cancer, immune, and autoimmune disorders and
 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 the antibodies and fragments of the antibodies described in the method
 of the invention.

Sequence 253 AA;

Query Match 86.2%; Score 50; DB 23; Length 253;
 Best Local Similarity 80.0%; Pred. No. 0.72;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
 |||||:
 Db 26 GYSFTDYVIH 35

RESULT 10

AAE15811

ID AAE15811 standard; Protein; 112 AA.

XX AAE15811;

AC AAE15811;

DT 26-MAR-2002 (first entry)

XX Human mAb 12B1 heavy chain variable region (VH).

DE Human; sialoadhesin factor-3; SAP-3; therapy; cancer; inflammation;
 XX autoimmunity; allergy; asthma; infection; central nervous system; CNS;
 KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;

RESULT 8

AAAB49746

ID AAB49746 standard; protein; 120 AA.

XX AAB49746;

DT 17-APR-2001 (first entry)

XX Anti-PP4/heparin complex antibody heavy chain amino acid sequence.

DE Antibody; platelet factor 4; heparin; PP4/heparin complex; mouse; HIT;

XX heparin induced thrombocytopaenia; heparin induced thrombosis; HIT.

OS Mus musculus.

PN WO200104159-A1.

XX 18-JAN-2001.

PD 13-JUL-2000; 2000WO-US19000.

XX 13-JUL-1999; 99US-0143536.

PR (SCTE-) SCI & TECHNOLOGY CORP @UNN.

PA Arepally G, Kiesel W, Kamei K, Kamei S;

PI WPI; 2001-138321/14.

XX N-PSDB; AAF29245.

XX Composition for the diagnosis and treatment of heparin induced

PT thrombocytopenia/thrombosis, comprises an antibody that preferentially

PT binds with a Platelet Factor 4/heparin complex -

XX Claim 5; Fig 7A; 80pp; English.

This invention relates to a composition comprising a monoclonal antibody
 which binds specifically with a Platelet Factor 4 (PF4)/heparin complex.
 The antibody preferentially binds to the complex relative to the binding
 of the antibody with either of the components alone. Methods are included
 for the production of the antibody and its use in the diagnosis of
 various diseases. The composition can be used for diagnosing heparin
 induced thrombocytopaenia/thrombosis, HIT/HITT. The composition can also
 be used for assessing the level of a polyclonal antibody that binds
 specifically within a bodily fluid or tissue sample. The present sequence
 represents the amino acid sequence of the heavy chain of the
 anti-PP4/heparin complex antibody of the invention.

Sequence 120 AA;

Query Match 86.2%; Score 50; DB 22; Length 120;
 Best Local Similarity 80.0%; Pred. No. 0.33;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
 |||||:
 Db 26 GYTFTNYFIY 35

RESULT 9

ABP45515

ID ABP45515 standard; Protein; 253 AA.

XX ABP45515;

DT 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1526.

DE Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW haematopoietic development; anaemia; chemoprotective agent; cytostatic; immunoglobulin; complementarity determining region; CDR; protozoacide;
 KW antinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;
 KW fungicide; neuroprotective; heavy chain variable region; VH; mAb;
 KW monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 31..35 /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 50..66 /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 99..102 /label= CDR
 FT /note= "Complementarity determining region"
 FT
 PN WO200190193-A1.
 XX
 XX 29-NOV-2001.
 XX
 XX 24-MAY-2001; 2001WO-US16864.
 XX
 XX 24-MAY-2000; 2000US-0577930.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Abrahamson JA, Kikly KK;
 PI
 XX WPI; 2002-083094/11.
 DR N-PSDB; AAD25486.
 XX
 XX Novel monoclonal antibody that binds to human sialoadhesin factor-3 for
 PT treating or preventing cancer, inflammation, autoimmunity, allergy,
 PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections
 PT
 XX Claim 20; Fig 1; 69pp; English.
 XX
 CC The invention relates to monoclonal antibodies that bind to human
 CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or
 CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central
 CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple
 CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections
 CC and for modulating an immune response in a mammal, where the immune
 CC response is downregulated or enhanced. SAF-3 antibody is useful as
 CC diagnostic and therapeutic reagents, to subcharacterise cell populations
 CC during haematopoietic development, to treat anaemia, as a diagnostic
 CC marker to distinguish between different forms of cancer, to purge bone
 CC marrow ex vivo of cancer cells expressing SAF-3, as a tool to aid in the
 CC ex vivo expansion (proliferation and/or differentiation) of
 CC haematopoietic progenitor cells expressing SAF-3, as a stimulus in vivo
 CC for stem cell mobilisation into the periphery and as an vivo
 CC chemoprotective agent. Protein comprising immunoglobulin complementarity
 CC determining region (CDR) of SAF-3 antibody and its nucleic acid is
 CC useful to configure screening methods for detecting the effect of added
 CC compounds on the production of mRNA and polypeptide in cells.
 CC The present sequence is human monoclonal antibody (mAb) 12B1 heavy
 CC chain variable region (VH) which binds to SAF-3.
 XX
 SQ Sequence 112 AA;
 Query Match 84.5%; Score 49; DB 23; Length 112;
 Best Local Similarity 90.0%; Pred. No. 0.45;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYSFTDYFIY 10
 ID AAW71288 standard; Protein; 117 AA.
 XX
 DB 26 GYFTDYNYI 35
 QY 1 GYSFTDYFIY 10
 ID AAW71288 standard; Protein; 117 AA.
 XX
 AC AAW71288;
 XX

RESULT 11
 AAG80197
 ID AAG80197 standard; peptide; 114 AA.
 XX
 AC AAG80197;
 XX
 XX 22-JAN-2002 (first entry)
 XX
 XX Human gp96 Ab clone G12D variable heavy chain framework region F1-FR4.
 DE
 XX Antibody; heavy chain; variable region; human; gp96; cytostatic;
 KW framework region; antibacterial; virucide; fungicide; FRI; FR4;
 KW protozoacide; tumour; autologous immunization; anti-idiotypic.
 XX
 OS Homo sapiens.
 XX
 XX DE10019967-A1.
 PN
 XX 25-OCT-2001.
 XX
 XX 20-APR-2000; 2000DE-1019967.
 PF
 XX 20-APR-2000; 2000DE-1019967.
 PR
 XX (FENN-) FENNING BIOMED GMBH.
 PA
 XX Terness P, Kleist C, Opelz G, Welschhof M, Arnold-Schild D;
 PI Schild H, Rammensee H;
 XX
 XX WPI; 2002-018649/03.
 DR
 XX New recombinant antibody specific for native gp96, useful for isolating
 PT gp96 as complex with endogenous peptides, used for autologous
 PT immunotherapy of e.g. tumor
 PT
 XX Claim 4; Page 15-16; 28pp; German.
 PS
 XX This invention describes a novel recombinant antibody (Ab) that binds
 CC native gp96. The product of the invention has cytostatic, antibacterial,
 CC virucide, fungicide and protozoacide activity. Complexes of gp96 with the
 CC peptides of the invention induce an immune response (cytotoxic T cells)
 CC specific for the associated peptides. Ab are used for purification or
 CC labeling of gp96, including intact complexes (C) with peptides (I), from
 CC small amounts of tumour or infected cells. (C) are useful: (i) in human
 CC or veterinary medicine for autologous immunization, for treating tumours
 CC and infections (by viruses, bacteria, mycoplasma, fungi and parasites
 CC (protozoa)); and (ii) for raising anti-idiotypic antibodies. Ab make
 CC possible isolation of very pure gp96 in native form, even from small
 CC tumour samples, in a one-step chromatographic process that does not
 CC require concanavalin A (as used in known processes and which may
 CC contaminate the final product by bleeding from the column). This sequence
 CC represents the variable heavy chain framework region FRI-FR4 fragment
 CC of the antibody raised against human gp96 described in the method of the
 CC invention.
 XX
 SQ Sequence 114 AA;
 Query Match 84.5%; Score 49; DB 23; Length 114;
 Best Local Similarity 70.0%; Pred. No. 0.46;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYSFTDYFIY 10
 ID AAW71288 standard; Protein; 117 AA.
 XX
 DB 26 GYFTDYNYI 35
 QY 1 GYSFTDYFIY 10
 ID AAW71288 standard; Protein; 117 AA.
 XX
 AC AAW71288;
 XX


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XX OS Mus sp.
XX OS US2001014328-A1.
XX PN 16-AUG-2001.
XX PD 26-JAN-2001; 2001US-0772120.
XX PF 10-JUL-1997; 97US-0890011.
XX PR 11-JUL-1996; 96US-0678194.
XX PR 11-JUL-1996; 96US-0678194.
XX PA (MEDE-) MEDERAX INC.
XX PI Deo YM, Graziano R, Keler T;
XX PI WPI: 2001-529092/58.
XX DR N-PSDB; AAD15263.
XX DR
XX PT New multispecific binding molecule, useful for treating cancer and
XX PT infections caused by bacteria, virus, fungi or protozoa, comprises
XX PT binding determinant for Fc alpha receptor and binding determinant for
XX PT target antigen.
XX PS Claim 18; Fig 28; 54pp; English.
XX CC
XX CC The present invention relates to multispecific binding molecules,
XX CC comprising a first binding determinant which binds an Fc alpha receptor,
XX CC or a functional fragment of antibody A77 and a second binding
XX CC determinant which binds one or more target antigens on a cancer cell or
XX CC on a pathogen (infected cell). The specific and multispecific molecules
XX CC can be used as therapeutic agents to harness the cytotoxicity and
XX CC phagocytosis capabilities of white blood cells, enhancing the attack of
XX CC these cells against cancer cells, cells of infectious microorganisms and
XX CC cells infected with pathogens. The multispecific binding molecules may
XX CC also be used to treat variety of diseases such as cancer (e.g. breast,
XX CC ovarian, testicular, prostate, lung, brain, colon or lymphatic system),
XX CC pathogenic infections such as viral (human immunodeficiency virus),
XX CC protozoan (e.g. Toxoplasma gondii), fungal (e.g. Candida albicans) and
XX CC bacterial (e.g. Staphylococcus aureus, S. haemolyticus and
XX CC Mycobacterium tuberculosis) and autoimmune diseases. These may also be
XX CC used as vaccine against diseases and cancer antigen or cancer found on
XX CC a pathogen or a cell infected by a pathogen. The methods can be used to
XX CC enhance or reinforce the immune response to an antigen, for the
XX CC treatment of acute and chronic infections, such as hepatitis and
XX CC acquired immunodeficiency syndrome (AIDS). The present sequence is
XX CC murine heavy chain variable (VH) region of A77 anti-Fc alpha R antibody.
XX CC
XX CC Sequence 142 AA;
XX CC
XX CC Query Match 82.8%; Score 48; DB 22; Length 142;
XX CC Best Local Similarity 80.0%; Pred. No. 0.86;
XX CC Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX CC
XX CC QY 1 GYSFTDYFIY 10
XX CC |||||!|:
XX CC Db 45 GYSFTDYIIF 54
XX CC
XX CC RESULT 15
XX CC AAB74622
XX CC ID AAB74622 standard; Protein; 142 AA.
XX CC
XX CC AC AAB74622;
XX CC
XX CC 22-MAY-2001 (first entry)
XX CC
XX CC A77 anti-Fc-alpha-R antibody VH region protein SEQ ID NO:8.
XX CC
XX CC Murine; human; immunoglobulin G1; IgG1; A77 anti-Fc-alpha-R antibody;
XX CC cytosstatic; antibacterial; antifungal; antiviral; antiparasitic;
XX CC cancer; pathogen; infection; vaccine.
XX CC

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OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX XX US6193966-B1.
XX PN 27-FEB-2001.
XX PD
XX PF 10-JUL-1997; 97US-0890011.
XX PR 11-JUL-1996; 96US-0678194.
XX PR 11-JUL-1996; 96US-0678194.
XX PA (MEDE-) MEDERAX INC.
XX PI Deo YM, Graziano R, Keler T;
XX PI WPI: 2001-243397/25.
XX DR N-PSDB; AAF74892.
XX DR
XX PT Selectively eliminating cancer cell in vivo by administering bispecific
XX PT protein comprising binding determinants that bind Fc alpha receptor
XX PT without being blocked by IgA and target antigen, respectively on the
XX PT cell.
XX PS Claim 16; Column 47-50; 55pp; English.
XX CC
XX CC The present invention describes a method for selectively eliminating a
XX CC cell in a subject involving administering a bispecific protein or peptide
XX CC (I) comprising first and second binding determinants (Bb1, Bb2) which
XX CC bind to the Fc-alpha receptor (FCR) without being blocked by
XX CC immunoglobulin A (IgA), and target antigen (Ag) on the cell,
XX CC respectively. (I) has cytostatic, antibacterial, antifungal, antiviral
XX CC and antiparasitic activities, and can be used for the selective
XX CC elimination of cancer cells and pathogen infected cells, and in vaccine
XX CC production. The method selectively eliminates a cell, a cancer cell from
XX CC cancers of breast, ovary, testis, lung, colon, rectum, pancreas, liver,
XX CC central nervous system, head and neck, kidney, bone, blood or lymphatic
XX CC system by administering (I) which comprises Bb1 that binds to FCR, and
XX CC Bb2 that binds to a target antigen, a cancer cell antigen such as a
XX CC member of the human epidermal growth factor (EGF)-like receptor family,
XX CC preferably an EGF receptor. Alternately, Bb2 binds to the cancer cell
XX CC antigen such as HER-2/neu or HER-3, HER-4, a heterodimeric receptor
XX CC comprised of at least one HER subunit, or a cancer cell antigen such as
XX CC carcinoembryonic antigen, gastrin releasing peptide receptor antigen or
XX CC mucine tumour antigen TAG72. Optionally Bb2 of (I) binds to a target
XX CC antigen, an antigen from a pathogen (bacteria, fungi (preferably
XX CC Candida sp., protozoa or virus) infected cell, (I) which comprises Bb1
XX CC and an antigen, preferably from disease organisms, infected cells, from
XX CC gene products of disease organisms or from cancer cells is useful for
XX CC vaccination purposes against diseases and cancers. The present sequence
XX CC represents the A77 anti-Fc-alpha-R antibody VH region, which is given in
XX CC the exemplification of the present invention.
XX CC
XX CC Sequence 142 AA;
XX CC
XX CC Query Match 82.8%; Score 48; DB 22; Length 142;
XX CC Best Local Similarity 80.0%; Pred. No. 0.86;
XX CC Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX CC
XX CC QY 1 GYSFTDYFIY 10
XX CC |||||!|:
XX CC Db 45 GYSFTDYIIF 54
XX CC
XX CC Search completed: March 10, 2003, 16:56:57
XX CC Job time : 29.2759 secs

```

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 48.069 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-7

Perfect score: 97

Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	17	21	AAV44593
2	97	100.0	113	21	AAV44588
3	97	100.0	137	21	AAV44600
4	97	100.0	237	21	AAV44595
5	97	100.0	243	21	AAV44596
6	76	78.4	110	20	AAW84099
7	76	78.4	117	20	AAW84093
8	76	78.4	117	20	AAW84097
9	74	76.3	236	15	AAW45442
10	74	76.3	237	17	AAW94020

11	74	76.3	237	18	AAW15185	Single-chain anti-
12	74	76.3	237	21	AAE19059	Amino acid sequenc
13	71	73.2	17	23	AAE15814	Human mAb 12B1 VH
14	71	73.2	98	13	AAE27008	Hypercalcaemia age
15	71	73.2	108	16	AAE79243	Heavy chain variab
16	71	73.2	112	23	AAE15811	Human mAb 12B1 hea
17	71	73.2	116	13	AAE27010	Hypercalcaemia age
18	71	73.2	116	18	AAW22418	Reshaped human AUK
19	71	73.2	135	13	AAE29016	pUC-RVh-1220b. Sy
20	71	73.2	135	13	AAE29017	pUC-RVh-1220d. Sy
21	71	73.2	135	13	AAE28669	p12-h2. Synthetic
22	70	72.2	119	13	AAE25730	Humanised VH regio
23	70	72.2	119	22	AAE69679	Murine CMV5 antibo
24	70	72.2	119	22	AAE69680	Humanised CMV5 ant
25	70	72.2	119	22	AAE69692	Human Wol antibody
26	70	72.2	138	22	AAE69688	Murine CMV5 antibo
27	70	72.2	243	15	AAE60781	Fv(GP-4) immunosup
28	69	71.1	118	20	AAE52755	Anti-tissue factor
29	69	71.1	118	20	AAE52756	Anti-tissue factor
30	69	71.1	118	20	AAE52759	Anti-tissue factor
31	69	71.1	118	20	AAE52760	Anti-tissue factor
32	69	71.1	120	22	AAE78737	Phosphonate ester
33	69	71.1	136	17	AAW06446	HuMc3 VH region BR
34	69	71.1	136	17	AAW06442	HuMc3 VH region.
35	68	70.1	17	22	AAE62862	Anti-SAF-1 antibod
36	68	70.1	17	23	AAU72830	Anti-NKG2D hybrido
37	68	70.1	117	23	AAU72830	Anti-NKG2D hybrido
38	68	70.1	120	22	AAE62860	Anti-SAF-1 monoclo
39	68	70.1	273	15	AAE52865	Anti-influenza N10
40	68	70.1	507	23	AAU72858	8G7C10x4-7 bispeci
41	67	69.1	115	19	AAW39812	Variable domain of
42	67	69.1	119	20	AAE21819	11E10 antibody hea
43	67	69.1	129	13	AAE25959	ICAM-1 inhibiting
44	67	69.1	139	14	AAE38259	Chimeric 128.1 VH,
45	67	69.1	153	12	AAE11597	Murine monoclonal

ALIGNMENTS

RESULT 1

AAV44593

ID AAV44593 standard; Protein: 17 AA.

XX AC AAV44593;

XX AC AAV44593;

XX DT 04-APR-2000 (first entry)

XX DE Mouse anti-IL-18 antibody VH complementarity-determining region-2.

XX DE Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;
complementarity-determining region; CDR; hybridoma #125-2H; mouse;
monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;
immunosuppressive; leucocytopoietic; antiallgic; antipyretic;
antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;
inflammatory disorder; immunoreaction.

XX OS Mus musculus.

XX PN EP974600-A2.

XX PD 26-JAN-2000.

XX PF 24-JUN-1999; 99EP-0304977.

XX PR 24-JUN-1998; 98JP-0177580.

XX PR 12-OCT-1998; 98JP-0289044.

XX PR 22-DEC-1998; 98JP-0365023.

XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX XX

DR WPI: 2000-118341/11.
 DR N-PSDB; AA249540.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Claim 7; Page 19; 36pp; English.
 XX
 CC The present protein sequence is a complementarity-determining region
 CC (CDR) of mouse anti-Interleukin-18 antibody heavy chain variable region
 CC (VH) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
 CC sequence can be used in the production of recombinant monoclonal antibody
 CC #125-2HmAb, which is capable of neutralizing biological activities of
 CC interleukin-18. The antibody has antinflammatory, immunosuppressive,
 CC leucocytopenic, antiallergic, antipyretic, antiallergic and hepatotropic
 CC activity and can be used for prevention and treatment of autoimmune
 CC diseases, immunopathies and inflammatory disorders caused by excessive
 CC immunoreaction.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 97; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.4e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIDPYNGDTSYNQKFRD 17
 Db 1 DIDPYNGDTSYNQKFRD 17
 RESULT 2
 AAY44588
 ID AAY44588 standard; Protein; 113 AA.
 XX
 AC AAY44588;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse anti-IL-18 antibody heavy chain variable region.
 XX
 KW Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;
 KW hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18;
 KW antinflammatory; immunosuppressive; leucocytopenic; antiallergic;
 KW antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease;
 KW immunopathy; inflammatory disorder; immunoreaction.
 XX
 OS Mus musculus.
 XX
 PN EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 PF 24-JUN-1999; 99EP-0304977.
 XX
 PR 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX
 DR WPI: 2000-118341/11.
 DR N-PSDB; AA249535.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Claim 5; Page 17-18; 36pp; English.
 XX
 CC The present protein sequence is the mouse anti-Interleukin-18 antibody

CC heavy chain variable region (VH) encoded by cDNA derived from hybridoma
 CC #125-2H. The nucleotide sequence is used in the production of recombinant
 CC monoclonal antibody #125-2HmAb, which is capable of neutralising
 CC biological activities of interleukin-18. The antibody has antiallgic,
 CC antinflammatory, immunosuppressive, leucocytopenic, antipyretic,
 CC antiallergic and hepatotropic activity and can be used for prevention and
 CC treatment of autoimmune diseases, immunopathies and inflammatory
 CC disorders caused by excessive immunoreaction.
 XX
 SQ Sequence 113 AA;
 Query Match 100.0%; Score 97; DB 21; Length 113;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIDPYNGDTSYNQKFRD 17
 Db 50 DIDPYNGDTSYNQKFRD 66
 RESULT 3
 AAY44600
 ID AAY44600 standard; Protein; 137 AA.
 XX
 AC AAY44600;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse heavy chain variable region encoded by PCR B product.
 XX
 KW Mouse heavy chain variable region; VH; variable region heavy chain;
 KW interleukin-18; immunopathies; inflammatory disorder; autoimmune disease;
 KW mouse; anti-allergic; anti-inflammatory; immunosuppressive;
 KW hematopoietic; leucocytopenic; antiallgic; antipyretic.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PN EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 PF 24-JUN-1999; 99EP-0304977.
 XX
 PR 24-JUN-1998; 98JP-0177580.
 PR 12-OCT-1998; 98JP-0289044.
 PR 22-DEC-1998; 98JP-0365023.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
 XX
 DR WPI: 2000-118341/11.
 DR N-PSDB; AA249549.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Disclosure; Page 29-30; 32pp; English.
 XX
 CC The present sequence is the mouse heavy chain variable region. This was
 CC encoded by a recombinant DNA is derived from PCR B which amplifies
 CC antibody heavy chain variable region (VH). The transformant produced
 CC using the VH gene was used transform competent E. coli cells. The peptide
 CC produced by transformants neutralises interleukin-18. This is useful for
 CC treating and preventing immunopathies, inflammatory disorders and
 CC autoimmune diseases which are caused by excessive immunoreaction. The
 CC peptide has anti-allergic, anti-inflammatory, immunosuppressive,
 CC hematopoietic, leucocytopenic, antiallgic, antipyretic and hepatic
 CC -function improving activities.
 XX
 SQ Sequence 137 AA;

Query Match 100.0%; Score 97; DB 21; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
Db 69 DIDPYNGDTSYNQKFRD 85
|||||

RESULT 4
AA44595
ID AAY44595 standard; Protein; 237 AA.

XX AC AAY44595;

XX 04-APR-2000 (first entry)

DE EscFv#125-2H recombinant protein.

XX EscFv#125-2H recombinant protein; interleukin-18; mouse;
KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.

OS Mus musculus.

XX Synthetic.

XX Key Location/Qualifiers

FT Domain 1..113

FT /note= "Heavy chain variable region"

FT 114..130

FT /note= "Glycine-serine linker"

FT 131..237

FT /note= "Light chain variable region"

FT EP974600-A2.

XX 26-JAN-2000.

XX 24-JUN-1999; 99EP-0304977.

XX 24-JUN-1998; 98JP-0177580.

XX 12-OCT-1998; 98JP-0289044.

XX 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

XX N-PSDB; AA4459542.

XX New artificially produced peptide for neutralizing biological activity

XX of interleukin-18, useful for treating and preventing immunopathies,

XX inflammatory disorders and autoimmune diseases -

XX Claim 8; Page 19-20; 32pp; English.

XX The present sequence is EscFv#125-2H protein encoded by recombinant cDNA

XX pEscFv#125-2H for neutralising interleukin-18. The protein is produced

XX from hybridoma #125-2H by transforming pEscFv#125-2H in competent

XX E. coli cells. This is useful for treating and preventing immunopathies,

XX inflammatory disorders and autoimmune diseases which are caused by

XX excessive immunoreaction. The protein has anti-allergic,

XX anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,

XX antialgic, antipyretic and hepatic-function improving activities.

XX Sequence 237 AA;

XX Query Match 100.0%; Score 97; DB 21; Length 237;

XX Best Local Similarity 100.0%; Pred. No. 8.4e-08;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17
Db 50 DIDPYNGDTSYNQKFRD 66
|||||

RESULT 5

AA44596

ID AAY44596 standard; Protein; 243 AA.

XX AC AAY44596;

XX 04-APR-2000 (first entry)

DE EscFv#125-2H recombinant protein.

XX EscFv#125-2H recombinant protein; interleukin-18; mouse;

KW immunopathies; inflammatory disorder; autoimmune disease; anti-allergic;

KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;

KW antialgic; antipyretic.

XX Mus musculus.

OS Synthetic.

XX Key Location/Qualifiers

FT Domain 1..113

FT /note= "Heavy chain variable region"

FT 114..130

FT /note= "Glycine-serine linker"

FT 131..237

FT /note= "Light chain variable region"

FT EP974600-A2.

XX 26-JAN-2000.

XX 24-JUN-1999; 99EP-0304977.

XX 24-JUN-1998; 98JP-0177580.

XX 12-OCT-1998; 98JP-0289044.

XX 22-DEC-1998; 98JP-0365023.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

XX N-PSDB; AA4459543.

XX New artificially produced peptide for neutralizing biological activity

XX of interleukin-18, useful for treating and preventing immunopathies,

XX inflammatory disorders and autoimmune diseases -

XX Claim 8; Page 20-21; 32pp; English.

XX The present sequence is EscFv#125-2H protein encoded by

XX recombinant cDNA pEscFv#125-2H for neutralising interleukin-18. The

XX protein is produced from hybridoma #125-2H by transforming

XX pEscFv#125-2H in competent E. coli cells. There are six histidine

XX residues positioned after the light chain variable region. This protein

XX is useful for treating and preventing immunopathies, inflammatory

XX disorders and autoimmune diseases which are caused by excessive

XX immunoreaction. The protein has anti-allergic, anti-inflammatory,

XX immunosuppressive, hematopoietic, leukocytopoietic, antialgic,

XX antipyretic and hepatic-function improving activities.

XX Sequence 243 AA;

XX Query Match 100.0%; Score 97; DB 21; Length 243;

XX Best Local Similarity 100.0%; Pred. No. 8.7e-08;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFRD 17

Db 50 DIDPYNGDTSYNQKFRD 66
 |||
 50 DIDPYNGDTSYNQKFRD 66

RESULT 6
 AAW84099
 ID AAW84099 standard; Protein; 110 AA.

XX AC AAW84099;

XX DT 15-MAR-1999 (first entry)

XX DE Vitronectin alpha-v beta-3 MAb VH.

XX KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 angiogenesis; diabetic retinopathy; inflammation;
 macular degeneration; osteoporosis; Paget's disease;
 hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX OS Mus sp.

XX PN WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI; 1999-034590/03.

XX DR N-PSDB; AAV1801.

XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 immunotherapeutic treatment of e.g. diabetic retinopathy,
 inflammatory disorders, atherosclerosis, restenosis, cancers or
 osteoporosis

XX PS Example 13; Page 63; 97pp; English.

XX CC This is the amino acid sequence of the region of the murine
 monoclonal antibody (MAb) D12 heavy chain variable region (VH)
 that is altered in humanised D12 VH (see also AAW84097). A
 synthetic gene (see AAW81901) encoding the protein was prepared
 from synthetic oligonucleotides and used to prepare an expression
 vector for humanised D12 VH. D12 is an anti-human alpha-v beta-3
 vitronectin receptor MAb. Humanised D12 MAb can be used for
 passive immunotherapy of disorders mediated by the alpha-v beta-3
 vitronectin receptor, e.g. restenosis and angiogenic associated
 diseases.

XX SQ Sequence 110 AA;

Query Match 78.4%; Score 76; DB 20; Length 110;
 Best Local Similarity 86.7%; Pred. No. 9.5e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16

Db 49 IDPYNGDTFFYNQKFK 63

RESULT 7

AAW84093

ID AAW84093 standard; Protein; 117 AA.

XX AC AAW84093;

XX

DT 15-MAR-1999 (first entry)
 XX DE Murine vitronectin alpha-v beta-3 receptor MAB VH region.

XX KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 angiogenesis; diabetic retinopathy; inflammation;
 macular degeneration; osteoporosis; Paget's disease;
 hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT Region 31..35

XX FT /label= CDR1

XX FT Region 50..66

XX FT /label= CDR2

XX FT Region 99..106

XX FT /label= CDR3

XX PN WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI; 1999-034590/03.

XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 immunotherapeutic treatment of e.g. diabetic retinopathy,
 inflammatory disorders, atherosclerosis, restenosis, cancers or
 osteoporosis

XX PS Example 13; Page 56; 97pp; English.

XX CC This is the amino acid sequence of the heavy chain variable region
 (VH) of the anti-human alpha-v beta-3 vitronectin receptor murine
 monoclonal antibody D12, as deduced from isolated cDNA (see
 AAV71797). D12 VH and VL (see AAW84094) show sequence similarity
 to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see
 AAW84096), respectively. Humanised VH (see AAW84097) and VL (see
 AAW84098) were constructed by combining the framework regions of the
 human V region consensus sequences with complementarity determining
 regions of D12 (keeping some preferred murine framework residues).
 The humanised antibodies are specifically reactive with the human
 alpha-v beta-3 protein receptor and capable of neutralising the
 receptor. They can be used for passive immunotherapy of a disorder
 mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
 disorders or angiogenic-related disorders, such as angiogenesis
 associated with diabetic retinopathy, atherosclerosis and
 restenosis, chronic inflammatory disorders, macular degeneration,
 rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
 diseases where bone resorption is associated with pathology such as
 osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
 of malignancy, osteolytic lesions produced by bone metastasis, bone
 loss due to immobilisation or sex hormone deficiency. They can also
 be used for targeted drug therapy, and for detection and diagnosis.

XX SQ Sequence 117 AA;

Query Match 78.4%; Score 76; DB 20; Length 117;

Best Local Similarity 86.7%; Pred. No. 0.0001;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16

|||||

CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis.

XX
 SQ Sequence 117 AA;

Query Match 78.4%; Score 76; DB 20; Length 117;
 Best Local Similarity 86.7%; Pred. No. 0.0001;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IDPYNQDTSYNOKFR 16
 DB 51 IDPYNQDTSYNOKFK 65

RESULT 9
 AAR45442
 ID AAR45442 standard; Protein; 236 AA.
 XX
 AC AAR45442;
 XX
 DT 21-JUL-1994 (first entry)
 XX
 DE Sequence of the single chain anti-erbB2 antibody, Ab no.23.
 XX
 KW Single chain anti-erbB1 antibody; cancer therapy; prevention;
 KW monoclonal antibody.
 XX
 OS Synthetic.
 XX
 PN W09400136-A.
 XX
 PD 06-JAN-1994.
 XX
 PF 21-OCT-1992; 92WO-US08545.
 XX
 PR 30-JUN-1992; 92US-0906555.
 XX
 PA (MOLE-) MOLECULAR ONCOLOGY INC.
 XX
 PI Kasprzyk PG, King CR;
 XX
 DR WPI; 1994-025878/03.
 DR N-PSDB; AAO55180.
 XX
 PT Treatment of malignancies over-expressing ERB-2 using at least
 PT 2 monoclonal antibodies which recognise different epitopes on
 PT gp185
 XX
 PS Example; Fig 7; 37pp; English.
 CC
 CC The source of human erbB-2 protein for the prodn. of antibodies no.
 CC 23 and 21 (AAO55180/R45442; AAO55181/R45443) is a NIH/3T3 cell
 CC engineered to express the human erbB-2 protein on its surface (N/
 CC erbB-2). Abs no. 21 and 23 are directed against the extracellular
 CC domain of gp185 erbB-2. Nude mice manipulated to produce rapidly
 CC growing tumours were used in a trial of the efficacy of the Abs. In
 CC animals given a combination of the 2 Abs, tumours completely
 CC regressed after 11 days.
 XX
 SQ Sequence 236 AA;

Query Match 76.3%; Score 74; DB 15; Length 236;
 Best Local Similarity 80.0%; Pred. No. 0.00047;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IDPYNQDTSYNOKFR 16
 DB 170 INPYNQDTSYNOKFK 184

RESULT 10
 AAR94020
 ID AAR94020 standard; Protein; 237 AA.

```

XX AAR94020;
XX 21-MAY-1996 (first entry)
XX Anti-erbB2 scFv.
XX Oncoprotein; erbB2; cell proliferation; tumour; cancer;
XX intracellular antibody homologue; single chain antibody; scFv;
XX gene therapy.
XX Synthetic.
XX WO9607321-A1.
XX 14-MAR-1996.
XX 23-AUG-1995; 95WO-US10740.
XX 06-JUN-1995; 95US-0468252.
XX 06-SEP-1994; 94US-0301339.
XX (UABR-) UAB RES FOUND.
XX Curiel DT, Deshane J;
XX WPI; 1996-171307/17.
XX N-PSDB; AAT17728.
XX Inhibition of proliferation or survival of, esp. malignant erbB2,
XX cells - by introducing nucleic acid mol. encoding antibody homologue
XX which is expressed and binds, pref. erbB2, protein intracellularly
XX Disclosure; Page 29-30; 48pp; English.
XX A nucleic acid comprises a first sequence encoding a signal peptide
XX (AAR94019) linked to a second sequence (AAT17728) encoding a single
XX chain Fv fragment (AAR94020) that binds a human erbB2 oncoprotein.
XX The anti-erbB2 scFv portion is obtained by PCR using e23scFv
XX plasmid as template. The signal peptide directs the scFv to the
XX endoplasmic reticulum. The nucleic acid is incorporated into a
XX plasmid or viral vector to facilitate expression of the scFv antibody
XX homologue within e.g. an epithelial carcinoma cell. Intracellular
XX expression of the homologue inhibits surface expression of erbB2 and
XX thereby inhibits cell proliferation and cell survival and decreases
XX tumorigenicity.
XX Sequence 237 AA;
Query Match 76.3%; Score 74; DB 17; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00048;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFR 16
Db 171 INPYNGDTNYNQKFK 185
RESULT 11
AAW15185
ID AAW15185 standard; Protein; 237 AA.
XX AAW15185;
XX 05-JUN-1997 (first entry)
XX Single-chain anti-erbB2 antibody e23(Fv).
XX Single chain antibody; variable region; light chain; heavy chain;
XX breast cancer; ovarian cancer; non-small cell lung carcinoma;
XX immunodiagnosis; treatment; cytotoxic agent; erbB-2.
XX Mus musculus.
OS

```

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OS Synthetic.
XX Key Location/Qualifiers
XX 108..121
XX /label= linker
XX US5587458-A.
XX 24-DEC-1996.
XX 07-OCT-1991; 91US-0772270.
XX 14-MAY-1993; 93US-0061092.
XX 07-OCT-1991; 91US-0772270.
XX 30-JUN-1992; 92US-0906555.
XX (ARON-) ARONEX PHARM INC.
XX Bird RE, Kasprzyk PG, King CR;
XX WPI; 1997-064831/06.
XX N-PSDB; AAT65006.
XX Single chain antibodies specific for erbB-2 protein, gp185 - with
XX labels or cytotoxin, useful for detection and treatment of tumour
XX cells expressing this protein
XX Claim 2; Columns 25-28; 28pp; English.
XX The present sequence represents a claimed single-chain antibody,
XX designated e23(Fv), which binds to erbB-2. Monoclonal antibody e23
XX was generated by immunising mice with N/erbB-2 cells overexpressing
XX the gp185 protein, removing spleen cells and producing hybridomas
XX by standard techniques. Messenger RNA coding for the anti-erbB-2
XX monoclonal antibody was isolated and converted to cDNA. Regions
XX coding for the heavy- and light- chain variable regions were then
XX amplified by PCR and joined via a sequence encoding a peptide
XX linker. The resulting single-chain antibody is useful for in vitro
XX diagnosis of tumour cells which overexpress the erbB-2 gp185
XX marker, e.g. breast, ovarian and non-small cell lung carcinomas,
XX and, when coupled to a cytotoxic agent, to treat such tumours.
XX Sequence 237 AA;
Query Match 76.3%; Score 74; DB 18; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.00048;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNQKFR 16
Db 171 INPYNGDTNYNQKFK 185
RESULT 12
AAW79059
ID AAW79059 standard; Protein; 237 AA.
XX AAW79059;
XX 20-JUN-2000 (first entry)
XX Amino acid sequence of anti-erbB2 scFv.
XX Anti-erbB2 scFv; erbB2; proliferation; cell death; cancer;
XX epithelial carcinoma; breast; ovary; gastrointestinal tract; lung;
XX salivary gland; oncogene; antibody.
XX Synthetic.
XX US6028059-A.
XX 22-FEB-2000.
XX

```


PF 24-JUN-1996; 96US-0668706.
 XX
 PR 06-SEP-1994; 94US-0301339.
 PR 06-JUN-1995; 95US-0468252.
 PA (UABR-) UAB RES FOUND.
 XX
 PI Deshane J, Curriel DT;
 XX WPI; 2000-316240/27.
 DR N-PSDB; AAZ98748.
 DR
 XX Controlling neoplastic cells which over express the transmembrane
 PT protein kinase receptor protein erbB2 for the treatment of cancer using
 PT intracellularly expressed antibodies .
 XX
 PS Example 1; Column 37-38; 40pp; English.
 XX
 CC This sequence represents the anti-erbB2 sFv amino acid sequence. The
 CC nucleotide sequence is used in the method of the invention which relates
 CC to killing or inhibiting a neoplastic cell expressing the oncoprotein
 CC erbB2. ErbB2 is a transmembrane kinase receptor protein that stimulates
 CC proliferation in a cell. The method comprises introducing into the cell,
 CC a nucleic acid molecule encoding an antibody homologue e.g. anti-erbB2
 CC sFv. The antibody is expressed intracellularly in the endoplasmic
 CC reticulum and causes the cell to die. The method may be used for treating
 CC cancers associated with over expression or amplification of the gene
 CC encoding oncoprotein erbB2. ErbB2 has been found to be over expressed in
 CC a variety of human epithelial carcinomas including malignancies of the
 CC breast, ovary, gastrointestinal tract, salivary gland and lung. In the
 CC case of ovarian and breast carcinomas, a direct correlation has been
 CC found between over expression of erbB2 and aggressive tumour growth and
 CC reduced patient survival. The antibody used in the method, targets
 CC immature intracellular forms of erbB2 causing disruption of surface
 CC expression of erbB2. The action of the antibody on cells that overexpress
 CC erbB2 causes the inhibition of both cell proliferation and cell survival.
 XX
 SQ Sequence 237 AA;
 Query Match 76.3%; Score 74; DB 21; Length 237;
 Best Local Similarity 80.0%; Pred. No. 0.00048;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IDPYNGDTSYNQKFR 16
 I:|||||:|||||:
 Db 171 INPYNGDTNYNQKFK 185
 RESULT 13
 AAEL15814
 ID AAEL15814 standard; peptide; 17 AA.
 XX
 AC AAEL15814;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human mAb 12B1 VH complementarity determining region (CDR) #2.
 XX
 KW Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;
 KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;
 KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;
 KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;
 KW immunoglobulin; complementarity determining region; CDR; protozoacide;
 KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;
 KW fungicide; neuroprotective; heavy chain variable region; VH; mAb;
 KW monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO200190193-A1.
 XX
 XX 29-NOV-2001.
 PD
 XX

PF 24-MAY-2001; 2001WO-US16864.
 XX
 PR 24-MAY-2000; 2000US-0577930.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Abrahamson JA, Kikly KK;
 XX WPI; 2002-083094/11.
 DR
 XX Novel monoclonal antibody that binds to human sialoadhesin factor-3 for
 PT treating or preventing cancer, inflammation, autoimmunity, allergy,
 PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections
 PT .
 XX
 PS Claim 13; Page 66; 69pp; English.
 XX
 CC The invention relates to monoclonal antibodies that bind to human
 CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or
 CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central
 CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple
 CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections
 CC and for modulating an immune response in a mammal, where the immune
 CC response is downregulated or enhanced. SAF-3 antibody is useful as
 CC diagnostic and therapeutic reagents, to subcharacterise cell populations
 CC during haematopoietic development, to treat anaemia, as a diagnostic
 CC marker to distinguish between different forms of cancer, to purge bone
 CC marrow ex vivo of cancer cells expressing SAF-3, as a tool to aid in the
 CC ex vivo expansion (proliferation and/or differentiation) of
 CC haematopoietic progenitor cells expressing SAF-3, as a stimulus in vivo
 CC for stem cell mobilisation into the periphery and as an vivo
 CC chemoprotective agent. Protein comprising immunoglobulin complementarity
 CC determining region (CDR) of SAF-3 antibody and its nucleic acid is
 CC useful to configure screening methods for detecting the effect of added
 CC compounds on the production of mRNA and polypeptide in cells.
 CC The present sequence is complementarity determining region of human
 CC monoclonal antibody (mAb) 12B1 heavy chain variable region (VH), which
 CC binds to SAF-3.
 XX
 SQ Sequence 17 AA;
 Query Match 73.2%; Score 71; DB 23; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.7e-05;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IDPYNGDTSYNQKFR 16
 I:|||||:|||||:
 Db 2 IDPYNDDTGYNQKFK 16
 RESULT 14
 AAR27008
 ID AAR27008 standard; peptide; 98 AA.
 XX
 AC AAR27008;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE Hypercalcaemia agent portion 1.
 XX
 DE Antihuman parathyroid hormone-related protein; monoclonal antibody;
 KW variable region; rodent/human chimeric MAb; constant region; PTHRp.
 KW
 XX Synthetic.
 OS
 XX JP04228089-A.
 PN
 XX 18-AUG-1992.
 PD
 XX 15-MAY-1991; 91JP-0110565.
 PF
 XX 15-MAY-1990; 90JP-0124581.
 PR

XX (KANF) KANEKA CORP.
 XX WPI; 1992-320987/39.
 XX Treatment and preventive agent for hypercalcaemia - contg. one of
 PT anti-human para-thyroid-hormone-related protein monoclonal antibody,
 PT a rodent or chimera monoclonal antibody, fused gene and cell
 PT line, etc.
 XX
 XX Disclosure; Page 13; 18pp; Japanese.
 XX The sequences given in AAR27008-11 are fragments which were used in
 CC the construction of an agent for the treating and prevention of
 CC hypercalcaemia. The agent contained a portion of the antihuman
 CC parathyroid hormone-related protein monoclonal antibody (antihuman
 CC PTHrP MAb). The MAb was used as the active component in the agent.
 CC The agent further comprises a rodent/human chimeric MAb which has a
 CC rodent variable region and a human constant region and recognises
 CC human PTHrP.
 XX
 XX Sequence 98 AA;

Query Match 73.28; Score 71; DB 13; Length 98;
 Best Local Similarity 80.0%; Pred. No. 0.00055;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 IDPYNGDTSYNQKFR 16
 I:||||| I|I|I|:
 Db 43 INPYNGDTFYNQKPK 57

RESULT 15
 AAR79243
 ID AAR79243 standard; Protein; 108 AA.
 XX
 AC AAR79243;
 XX
 XX 21-DEC-1995 (first entry)
 XX Heavy chain variable region for monoclonal antibody 5G4.
 DE
 XX Monoclonal antibody; heavy metal; mercury; variable region;
 KW heavy chain.
 XX
 OS Synthetic.
 XX
 FN W09520607-A.
 XX
 PD 03-AUG-1995.
 XX
 XX 27-JAN-1995; 95WO-US01199.
 XX
 XX 27-JAN-1994; 94US-0187407.
 PR
 XX (BION-) BIONEBRASKA INC.
 XX
 XX Lopez O, Wagner FW, Wylie DE;
 PT
 XX WPI: 1995-275415/36.
 DR
 DR N-PSDB; AAR97500.
 XX
 XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals
 XX
 XX Claim 13; Page 57; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of
 CC BALB/c mouse that had received multiple injections of mercuric ions
 CC reacted with glutathione to produce a mercuric ion coordinate
 CC covalent compound which was covalently bound to keyhole limpet
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,

CC 5B6 and 3E8) were producing MABs that were strongly positive
 CC against glutathione-mercuric ions but negative against glutathione
 CC without mercuric ions. RNA was isolated from hybridoma cells with
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
 CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
 CC were complementary to the 5' end of the CHI domain of the heavy
 CC chain expressed by the hybridoma of interest, or to the 5' and of
 CC the C kappa domain. Some of the primers used for cDNA synthesis are
 CC shown in AAR97511-097518. The primer used for cDNA synthesis of the
 CC variable region of a particular antibody polypeptide was also used
 CC for PCR amplification of that variable region, in conjunction with
 CC an appropriate V-region primer. In addition, the VH primer AAR97518
 CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
 CC of the PCR amplified nucleotides were determined. These are given
 CC in AAR97498-097510 and the deduced AA sequences in AAR79241-R79250 &
 CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
 CC and in the claims are different from the descriptions in the
 CC sequence listings. The descriptions in the sequence listings are
 CC used here.

XX
 SQ Sequence 108 AA;

Query Match 73.28; Score 71; DB 16; Length 108;
 Best Local Similarity 80.0%; Pred. No. 0.00061;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 IDPYNGDTSYNQKFR 16
 I:||||| I|I|I|:
 Db 45 INPYNGDTFYNQKPK 59

Search completed: March 10, 2003, 16:56:58
 Job time : 49.069 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:21 ; Search time 11.3103 Seconds
(without alignments)
47.125 Million cell updates/sec

Title: US-09-924-099-8

Perfect score: 21

Sequence: 1 GLRF 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	21 AAY44594	Mouse anti-IL-18 a
2	21	100.0	7	21 AAY91101	Human Kiss-1 PEPTI
3	21	100.0	8	21 AAY91099	Human Kiss-1 PEPTI
4	21	100.0	9	21 AAY91098	Human Kiss-1 PEPTI
5	21	100.0	10	21 AAY91097	Human Kiss-1 PEPTI
6	21	100.0	10	22 AAG95320	Human complementar
7	21	100.0	14	22 AAG96847	Human peptide #122
8	21	100.0	15	19 AAW59970	Phosphotransferase
9	21	100.0	15	21 AAY91096	Human Kiss-1 PEPTI
10	21	100.0	18	19 AAW66645	HSV-2 glycoprotein

11	21	100.0	18	19 AAW66646	HSV-2 glycoprotein
12	21	100.0	20	20 AAY26958	Human/rat TrkA pro
13	21	100.0	24	19 AAW36898	Leucine rich motif
14	21	100.0	24	19 AAW36901	Leucine rich motif
15	21	100.0	25	19 AAW40518	Human TrkA leucine
16	21	100.0	25	20 AAY40047	Peptide sequence d
17	21	100.0	30	19 AAW53267	Herpes simplex vir
18	21	100.0	32	20 AAY12540	Human 5' EST secre
19	21	100.0	34	22 ABG21915	Novel human diagno
20	21	100.0	34	22 AAG74972	Human colon cancer
21	21	100.0	38	22 AAB99240	Human pituitary ad
22	21	100.0	38	22 AAB99241	Human pituitary ad
23	21	100.0	38	22 AAB99242	Human pituitary ad
24	21	100.0	38	22 AAB99243	Human pituitary ad
25	21	100.0	38	22 AAB99244	Human pituitary ad
26	21	100.0	38	22 AAB99245	Human pituitary ad
27	21	100.0	38	22 AAB99246	Human pituitary ad
28	21	100.0	38	22 AAB99247	Human pituitary ad
29	21	100.0	38	22 AAB99248	Human pituitary ad
30	21	100.0	38	22 AAB99249	Human pituitary ad
31	21	100.0	38	22 AAB99250	Human pituitary ad
32	21	100.0	38	22 AAB99251	Human pituitary ad
33	21	100.0	38	22 AAB99253	Human pituitary ad
34	21	100.0	38	22 AAB99255	Human pituitary ad
35	21	100.0	38	22 AAB99256	Human pituitary ad
36	21	100.0	38	22 AAB99257	Human pituitary ad
37	21	100.0	38	22 AAB99258	Human pituitary ad
38	21	100.0	38	22 AAB99259	Human pituitary ad
39	21	100.0	38	22 AAB99260	Human pituitary ad
40	21	100.0	38	22 AAB99261	Human pituitary ad
41	21	100.0	38	22 AAB99262	Human pituitary ad
42	21	100.0	38	22 AAB99263	Human pituitary ad
43	21	100.0	38	22 AAB99264	Human pituitary ad
44	21	100.0	38	22 AAB99265	Human pituitary ad
45	21	100.0	38	22 AAB99266	Human pituitary ad

ALIGNMENTS

RESULT 1

AAY44594

ID AAY44594 standard; Protein; 4 AA.

AC AAY44594;

XX

DT 04-APR-2000 (first entry)

XX Mouse anti-IL-18 antibody VH complementarity-determining region-3.

DE Anti-Interleukin-18 antibody; IL-18; heavy chain variable region; VH;

XX Complementarity-determining region; CDR; hybirdoma #125-2H; mouse;

KW monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory;

KW immunosuppressive; leucocytopenic; antiallergic; antipyretic;

KW antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy;

KW inflammatory disorder; immunoreaction.

XX Mus musculus.

XX EP974600-A2.

PN 26-JAN-2000.

PD 24-JUN-1999;

XX 99EP-0304977.

XX 24-JUN-1998;

XX 98JP-0177580.

PR 12-OCT-1998;

 XX 98JP-0289044. || PR | 22-DEC-1998; | XX 98JP-0365023. |
XX	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
PA		
XX	Nishida Y, Okura T, Tanimoto T, Kurimoto M;	
PI		
XX		

DR WPI; 2000-118341/11.
 DR N-PSDB; AAZ49541.
 XX
 PT New artificially produced peptide for neutralizing biological activity
 PT of interleukin-18, useful for treating and preventing immunopathies,
 PT inflammatory disorders and autoimmune diseases -
 XX
 PS Claim 7; Page 19; 36pp; English.
 XX
 CC The present protein sequence is a complementarity-determining region
 CC (CDR) of mouse anti-interleukin-18 antibody heavy chain variable region
 CC (VH) encoded by cDNA derived from hybridoma #125-2H. The nucleotide
 CC sequence can be used in the production of recombinant monoclonal antibody
 CC #125-2HmAb, which is capable of neutralizing biological activities of
 CC interleukin-18. The antibody has antiinflammatory, immunosuppressive,
 CC leucocytopenetic, antialgic, antipyretic, antiallergic and hepatotropic
 CC activity and can be used for prevention and treatment of autoimmune
 CC diseases, immunopathies and inflammatory disorders caused by excessive
 CC immunoreaction.
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 1 GLRF 4
 1111
 1 GLRF 4

RESULT 2
 AAY91101
 ID AAY91101 standard; Peptide; 7 AA.
 XX
 AC AAY91101;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Human Kiss-1 PEPTIDE(48-54) amino acid sequence SEQ ID NO:21.
 XX
 KW G protein-coupled receptor protein; rOR7T175; hOR7T175; tumour;
 KW guanine nucleotide binding protein; cytosolic; anti-proliferative;
 KW cancer; diagnosis; Kiss-1.
 XX
 OS Homo sapiens.
 XX
 PN WO200024890-A1.
 XX
 PD 04-MAY-2000.
 XX
 PF 26-OCT-1999; 99WO-JP05905.
 XX
 PR 27-OCT-1998; 98JP-0305949.
 PR 04-FEB-1999; 99JP-0027710.
 PR 04-MAR-1999; 99JP-0057207.
 PR 29-SEP-1999; 99JP-0276225.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
 XX
 DR WPI; 2000-350732/30.
 DR N-PSDB; AAA39352.
 XX
 PT G protein coupled receptor protein, antibodies to it and a method of
 PT screening compounds which alter the binding of the receptor to its
 PT ligands for treatment of diseases including tumors -
 XX
 PS Example 3; Page 112; 114pp; Japanese.
 XX
 CC The present invention describes a human and a rat G protein-coupled
 CC receptor protein, designated hOR7T175 and rOR7T175 respectively. The

CC G protein-coupled receptor protein has cytostatic and anti-proliferative
 CC activities. The protein and antibodies raised against it are useful in
 CC the diagnosis, treatment and prevention of disorders with which the
 CC G protein-coupled receptor protein is associated, in particular for
 CC inhibition of the proliferation of cancers such as lung, kidney, liver,
 CC pancreas, colon, breast and ovary cancer. The protein is also used to
 CC identify ligands to it by their ability to bind to all or part of the
 CC sequence of the protein and for identifying compounds which affect the
 CC binding of the protein to its ligands. The present sequence represents
 CC a peptide derived from the human Kiss-1 protein, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 21; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 4 GLRF 7
 1111
 4 GLRF 7

RESULT 3
 AAY91099
 ID AAY91099 standard; Peptide; 8 AA.
 XX
 AC AAY91099;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Human Kiss-1 PEPTIDE(47-54) amino acid sequence SEQ ID NO:14.
 XX
 KW G protein-coupled receptor protein; rOR7T175; hOR7T175; tumour;
 KW guanine nucleotide binding protein; cytosolic; anti-proliferative;
 KW cancer; diagnosis; Kiss-1.
 XX
 OS Homo sapiens.
 XX
 PN WO200024890-A1.
 XX
 PD 04-MAY-2000.
 XX
 PF 26-OCT-1999; 99WO-JP05905.
 XX
 PR 27-OCT-1998; 98JP-0305949.
 PR 04-FEB-1999; 99JP-0027710.
 PR 04-MAR-1999; 99JP-0057207.
 PR 29-SEP-1999; 99JP-0276225.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
 XX
 DR WPI; 2000-350732/30.
 DR N-PSDB; AAA39351.
 XX
 PT G protein coupled receptor protein, antibodies to it and a method of
 PT screening compounds which alter the binding of the receptor to its
 PT ligands for treatment of diseases including tumors -
 XX
 PS Claim 23; Page 109; 114pp; Japanese.
 XX
 CC The present invention describes a human and a rat G protein-coupled
 CC receptor protein, designated hOR7T175 and rOR7T175 respectively. The
 CC G protein-coupled receptor protein has cytostatic and anti-proliferative
 CC activities. The protein and antibodies raised against it are useful in
 CC the diagnosis, treatment and prevention of disorders with which the
 CC G protein-coupled receptor protein is associated, in particular for
 CC inhibition of the proliferation of cancers such as lung, kidney, liver,
 CC pancreas, colon, breast and ovary cancer. The protein is also used to
 CC identify ligands to it by their ability to bind to all or part of the
 CC sequence of the protein and for identifying compounds which affect the

CC binding of the protein to its ligands. The present sequence represents
CC a specifically claimed peptide derived from the human Kiss-1 protein,
CC which is used in the exemplification of the present invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 21; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 5 GLRF 8

RESULT 4

AA91098

ID AA91098 standard; Peptide; 9 AA.

XX AC AA91098;

XX DT 11-SEP-2000 (first entry)

XX DE Human Kiss-1 PEPTIDE(46-54) amino acid sequence SEQ ID NO:13.

XX KW G protein-coupled receptor protein; rOT7rl75; hOT7rl75; tumour;
XX guanine nucleotide binding protein; cytostatic; anti-proliferative;
XX cancer; diagnosis; Kiss-1.

XX OS Homo sapiens.

XX PN WO200024890-A1.

XX PD 04-MAY-2000.

XX PF 26-OCT-1999; 99WO-JP05905.

XX PR 27-OCT-1998; 98JP-0305949.

XX PR 04-FEB-1999; 99JP-0027710.

XX PR 04-MAR-1999; 99JP-0057207.

XX PR 29-SEP-1999; 99JP-0276225.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;

XX WPI; 2000-350732/30.

XX DR N-PSDB; AAA39350.

XX PT G protein coupled receptor protein, antibodies to it and a method of
XX screening compounds which alter the binding of the receptor to its
XX ligands for treatment of diseases including tumors

XX PS Claim 23; Page 108; 114pp; Japanese.

XX The present invention describes a human and a rat G protein-coupled
XX receptor protein, designated hOT7rl75 and rOT7rl75 respectively. The
XX G protein-coupled receptor protein has cytostatic and anti-proliferative
XX activities. The protein and antibodies raised against it are useful in
XX the diagnosis, treatment and prevention of disorders with which the
XX G protein-coupled receptor protein is associated, in particular for
XX inhibition of the proliferation of cancers such as lung, kidney, liver,
XX pancreas, colon, breast and ovary cancer. The protein is also used to
XX identify ligands to it by their ability to bind to all or part of the
XX sequence of the protein and for identifying compounds which affect the
XX binding of the protein to its ligands. The present sequence represents
XX a specifically claimed peptide derived from the human Kiss-1 protein,
XX which is used in the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match

Best Local Similarity 100.0%; Score 21; DB 21; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 6 GLRF 9

RESULT 5

AA91097

ID AA91097 standard; Peptide; 10 AA.

XX AC AA91097;

XX DT 11-SEP-2000 (first entry)

XX DE Human Kiss-1 PEPTIDE(45-54) amino acid sequence SEQ ID NO:12.

XX KW G protein-coupled receptor protein; rOT7rl75; hOT7rl75; tumour;
XX guanine nucleotide binding protein; cytostatic; anti-proliferative;
XX cancer; diagnosis; Kiss-1.

XX OS Homo sapiens.

XX PN WO200024890-A1.

XX PD 04-MAY-2000.

XX PF 26-OCT-1999; 99WO-JP05905.

XX PR 27-OCT-1998; 98JP-0305949.

XX PR 04-FEB-1999; 99JP-0027710.

XX PR 04-MAR-1999; 99JP-0057207.

XX PR 29-SEP-1999; 99JP-0276225.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;

XX WPI; 2000-350732/30.

XX DR N-PSDB; AAA39349.

XX PT G protein coupled receptor protein, antibodies to it and a method of
XX screening compounds which alter the binding of the receptor to its
XX ligands for treatment of diseases including tumors

XX PS Claim 23; Page 108; 114pp; Japanese.

XX The present invention describes a human and a rat G protein-coupled
XX receptor protein, designated hOT7rl75 and rOT7rl75 respectively. The
XX G protein-coupled receptor protein has cytostatic and anti-proliferative
XX activities. The protein and antibodies raised against it are useful in
XX the diagnosis, treatment and prevention of disorders with which the
XX G protein-coupled receptor protein is associated, in particular for
XX inhibition of the proliferation of cancers such as lung, kidney, liver,
XX pancreas, colon, breast and ovary cancer. The protein is also used to
XX identify ligands to it by their ability to bind to all or part of the
XX sequence of the protein and for identifying compounds which affect the
XX binding of the protein to its ligands. The present sequence represents
XX a specifically claimed peptide derived from the human Kiss-1 protein,
XX which is used in the exemplification of the present invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 21; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 7 GLRF 10

RESULT 6

AAG95320
 ID AAG95320 standard; Peptide; 10 AA.
 XX
 AC AAG95320;
 XX
 DT 18-SEP-2001 (first entry)
 XX
 DE Human complementary peptide, SEQ ID NO: 1514.
 XX
 KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX
 OS Homo sapiens.
 XX
 PN WO200142277-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 13-DEC-2000; 2000WO-GB04776.
 XX
 PR 13-DEC-1999; 99GB-0029464.
 XX
 PA (PROT-) PROTEOM LTD.
 XX
 PI Roberts GW, Heal JR;
 XX
 DR WPI; 2001-408419/43.
 XX
 PT A set of peptide ligands consisting of specific complementary peptides
 PT to proteins encoded by genes of the human genome, useful in an assay
 PT for screening and identifying of one or more novel peptides which are
 PT drug candidates or pro-drugs -
 XX
 PS Example 4; Page 259; 646pp: English.
 XX
 CC The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 21; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 4 GLRF 7
 RESULT 7
 AAM96847
 ID AAM96847 standard; Peptide; 14 AA.
 XX
 AC AAM96847;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #122 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 OS Homo sapiens.
 XX

PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Disclosure; Page 3694; 4143pp: English.
 XX
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 21; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 6 GLRF 9
 RESULT 8
 AAW59970
 ID AAW59970 standard; peptide; 15 AA.
 XX
 AC AAW59970;
 XX
 DT 02-DEC-1998 (first entry)
 XX
 DE Phosphotransferase system inhibition peptide 14.
 XX
 KW Phosphotransferase system; PPS; inhibition; antimicrobial;
 KW phage display; hydrolysis; infectious disease; respiratory infection;
 KW diarrhoeal disease; tuberculosis; neonatal tetanus; whooping cough;
 KW phosphohydrolase.
 XX
 OS Synthetic.
 XX
 PN EP866075-A2.
 XX
 PD 23-SEP-1998.
 XX
 PF 02-FEB-1998; 98EP-0101704.
 PF 19-FEB-1997; 97EP-0102616.
 PR

XX (ARPI-) ARPIDA.
 XX
 XX
 PI Erni B;
 XX
 DR WPI: 1998-482931/42.
 XX
 XX Drug target system for specific new antimicrobial agents comprises
 PT uncoupling or inhibiting bacterial phosphotransferase system - used
 PT to treat infections e.g. respiratory infections, diarrhoeal
 PT diseases, tuberculosis and whooping cough
 XX
 XX
 PS Claim 8; Page 25; 25pp; English.
 XX
 CC This is the amino acid of a phosphotransferase system (PTS) inhibition
 CC peptide identified by phage display. It is used in the method of the
 CC invention as part of a drug target system for specific antimicrobials
 CC comprising uncoupling or inhibition of the bacterial PTS by using a
 CC phosphoryl group acceptor which is not part of the system and
 CC hydrolyses spontaneously or under the influence of non-specific
 CC endogenous phosphohydrolases or inhibiting the phosphotransferase
 CC system actively with chemical compounds which block or inactivate at
 CC least one of the enzymes of the phosphotransferase system. The
 CC peptides are used to treat infectious diseases e.g. respiratory
 CC infections, diarrhoeal diseases, tuberculosis, neonatal tetanus and
 CC whooping cough.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 21; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db | | | |
 1 GLRF 4
 RESULT 9
 AAY91096
 ID AAY91096 standard; Peptide; 15 AA.
 XX
 AC AAY91096;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Human Kiss-1 PEPTIDE(40-54) amino acid sequence SEQ ID NO:11.
 XX
 KW G protein-coupled receptor protein; rOT7T175; hOT7T175; tumour;
 KW guanine nucleotide binding protein; cytosolic; anti-proliferative;
 KW cancer; diagnosis; Kiss-1.
 XX
 OS Homo sapiens.
 XX
 PN WO200024890-A1.
 XX
 PD 04-MAY-2000.
 XX
 PF 26-OCT-1999; 99WO-JP05905.
 XX
 PR 27-OCT-1998; 98JP-0305949.
 PR 04-FEB-1999; 99JP-0027710.
 PR 04-MAR-1999; 99JP-0057207.
 PR 29-SEP-1999; 99JP-0276225.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Watanabe T, Terso Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;
 XX
 DR WPI: 2000-350732/30.
 DR N-PSDB; AAA39348.
 XX
 PT G protein coupled receptor protein, antibodies to it and a method of

PT screening compounds which alter the binding of the receptor to its
 XX ligands for treatment of diseases including tumors
 PS Claim 23; Page 107-108; 114pp; Japanese.
 XX
 CC The present invention describes a human and a rat G protein-coupled
 CC receptor protein, designated hOT7T175 and rOT7T175 respectively. The
 CC G protein-coupled receptor protein has cytostatic and anti-proliferative
 CC activities. The protein and antibodies raised against it are useful in
 CC the diagnosis, treatment and prevention of disorders with which the
 CC G protein-coupled receptor protein is associated, in particular for
 CC inhibition of the proliferation of cancers such as lung, kidney, liver,
 CC pancreas, colon, breast and ovary cancer. The protein is also used to
 CC identify ligands to it by their ability to bind to all or part of the
 CC sequence of the protein and for identifying compounds which affect the
 CC binding of the protein to its ligands. The present sequence represents
 CC a specifically claimed peptide derived from the human Kiss-1 protein,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 21; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db | | | |
 12 GLRF 15
 RESULT 10
 AAW66645
 ID AAW66645 standard; peptide; 18 AA.
 XX
 AC AAW66645;
 XX
 DT 30-NOV-1998 (first entry)
 XX
 DE HSV-2 glycoprotein G partial sequence (residues 231-248).
 XX
 KW Herpes simplex virus type 2; HSV-2 antibody; detection; HSV-1;
 KW multiply displayed peptide structure.
 XX
 OS Synthetic.
 OS Herpes simplex virus type 2.
 PN GB2323360-A.
 XX
 PD 23-SEP-1998.
 XX
 PF 14-JAN-1997; 97GB-0000660.
 XX
 PR 14-JAN-1997; 97GB-0000660.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Marsden HS;
 XX
 DR WPI: 1998-459516/40.
 XX
 PT New peptide compounds useful for detecting herpes simplex virus type
 PT 2 - can differentiate between herpes simplex virus type 1 and type 2
 PS Example 1; Page 10; 25pp; English.
 XX
 CC The invention relates to a multiply displayed peptide structure of
 CC formula [(X1)p-A-(X2)q-Sp]-n-Core. X1, X2 = 1-6 non-interfering amino
 CC acid residues; A = Glu, Phe, Glu, Ala, Gly, Asp, Gly, Pro, Glu
 CC Asp, Asp, Asp; Sp = spacer group extending outwardly from the core; n at
 CC least 4; and p, q = 0 or 1. The linkage between the core and the spacer
 CC may be chemical or physical. Peptides of this formula are used in the
 CC diagnosis of herpes simplex virus type 2 (HSV-2). The peptides can
 CC distinguish HSV-2 from HSV-1. A series of 67 peptides (AAW66624-W66690),

CC mostly 18 amino acids long, that spanned amino acids 21-699 of the
 CC predicted open reading frame of HSV gG2 were synthesised. The peptides
 CC were made as multiply displayed peptide structures of the invention and
 CC were screened against sera from HSV-1, HSV-2 antibody-positive
 CC individuals and from individuals having no laboratory evidence of HSV
 CC infection. From the results, peptide 55 (AAW66678) was considered a
 CC likely candidate for type specific serodiagnosis of HSV.

SQ Sequence 18 AA;

Query Match 100.0%; Score 21; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
 DB 15 GLRF 18
 ||||

RESULT 11
 AAW66646
 ID AAW66646 standard; peptide; 18 AA.
 XX AC AAW66646;
 XX DT 30-NOV-1998 (first entry)
 XX DE HSV-2 glycoprotein G partial sequence (residues 241-258).
 XX KW Herpes simplex virus type 2; HSV-2 antibody; detection; HSV-1;
 XX KW multiply displayed peptide structure.
 XX OS Synthetic.
 XX OS Herpes simplex virus type 2.
 XX FN GB2323360-A.
 XX PD 23-SEP-1998.
 XX PF 14-JAN-1997; 97GB-0000660.
 XX PR 14-JAN-1997; 97GB-0000660.
 XX PA (MEDI-) MEDICAL RES COUNCIL.
 XX PI Marsden HS;
 XX DR WPI; 1998-459516/40.
 XX PT New peptide compounds useful for detecting herpes simplex virus type
 PT 2 - can differentiate between herpes simplex virus type 1 and type 2
 XX PS Example 1; Page 10; 25pp; English.
 XX CC The invention relates to a multiply displayed peptide structure of
 CC formula (X1)p-A-(X2)q-Spin-Core. X1, X2 = 1-6 non-interfering amino
 CC acid residues; A = Glu Gly Phe Glu Ala Gly Asp Gly Glu Pro Glu
 CC Asp Asp Asp; Sp = spacer group extending outwardly from the core; n at
 CC least 4; and p, q = 0 or 1. The linkage between the core and the spacer
 CC may be chemical or physical. Peptides of this formula are used in the
 CC diagnosis of herpes simplex virus type 2 (HSV-2). The peptides can
 CC distinguish HSV-2 from HSV-1. A series of 67 peptides (AAW66624-W66690),
 CC mostly 18 amino acids long, that spanned amino acids 21-699 of the
 CC predicted open reading frame of HSV gG2 were synthesised. The peptides
 CC were made as multiply displayed peptide structures of the invention and
 CC were screened against sera from HSV-1, HSV-2 antibody-positive
 CC individuals and from individuals having no laboratory evidence of HSV
 CC infection. From the results, peptide 55 (AAW66678) was considered a
 CC likely candidate for type specific serodiagnosis of HSV.

SQ Sequence 18 AA;

Query Match 100.0%; Score 21; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 69;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
 DB 5 GLRF 8
 ||||

RESULT 12
 AAY26958
 ID AAY26958 standard; peptide; 20 AA.
 XX AC AAY26958;
 XX DT 21-DEC-1999 (first entry)
 XX DE Human/rat TrkA protein fragment amino acids 99-118.
 XX KW Human; TrkA; nerve growth factor; NGF; receptor; antibody; diagnosis;
 KW neurodegeneration; Alzheimer's disease; Parkinson's disease; cytoplasm;
 KW Huntington's disease; amyotrophic lateral sclerosis; gangliosidosis;
 KW nuclear translocation.
 XX OS Homo sapiens.
 XX OS Rattus sp.
 XX FN WO9948908-A2.
 XX PD 30-SEP-1999.
 XX PF 26-MAR-1999; 99WO-FR00716.
 XX PR 26-MAR-1998; 98FR-0004011.
 XX PA (CNRS) CENT NAT RECH SCI.
 XX PI Rudkin B;
 XX DR WPI; 1999-572168/48.
 XX PT New fragments of the TrkA receptor for nerve growth factor, for
 PT diagnosis, prevention and treatment of neurodegeneration -
 XX PS Claim 5; Page 14; 15pp; French.
 XX CC The invention relates to the use of a TrkA protein (the nerve growth
 CC factor (NGF) receptor (AAY26956)) or fragments (AAY26957-Y26963) of TrkA
 CC to raise antibodies to the TrkA polypeptide. The fragments especially
 CC cover amino acids (aa) 71-87, 125-141, 265-283, 379-392 or 382-417. The
 CC protein or fragments, also the 99-118 aa fragment of TrkA, and their
 CC related antibodies and nucleic acids are used for diagnosis, prevention
 CC and treatment of neurodegeneration, e.g. Alzheimer's, Parkinson's and
 CC Huntington's diseases, amyotrophic lateral sclerosis and GMI
 CC gangliosidosis, associated with abnormal regulation of TrkA. The protein
 CC can be used to raise specific antibodies and these used to determine
 CC cellular localization of TrkA and to provide information on the form of
 CC the receptor (and thus of NGF activity). Especially after
 CC internalization of TrkA, induced by NGF, only the extracellular receptor
 CC domain undergoes nuclear translocation, with the intracellular domain
 CC retained in the cytoplasm.

SQ Sequence 20 AA;

Query Match 100.0%; Score 21; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
 DB 4 GLRF 7
 ||||

RESULT 13

AAW36898
 ID AAW36898 standard; peptide; 24 AA.
 AC AAW36898;
 XX
 XX 01-APR-1998 (first entry)
 DT
 XX Leucine rich motif peptide of the human tyrosine kinase receptor A.
 DE
 XX Leucine rich motif; LRM2; extracellular domain;
 KW tyrosine kinase receptor A; neurotrophin binding region;
 KW neurotrophin activity agonist; neurotrophin activity antagonist.
 XX
 OS Homo sapiens.
 XX
 XX US5688911-A.
 PN
 XX 18-NOV-1997.
 PD
 XX 03-MAY-1995; 95US-0434198.
 PF
 XX 03-MAY-1995; 95US-0434198.
 PR
 XX (SCHN/) SCHNEIDER R.
 XX (WIND/) WINDISCH J M.
 PA
 XX Schneider R, Windisch JM;
 PI
 XX WPI; 1998-008037/01.
 DR
 XX Tyrosine kinase receptor peptide(s) - useful in screening assays for
 PT neurotrophin agonists and antagonists
 PS Claim 1; Column 13; 8pp; English.
 XX
 CC The present sequence represents a novel leucine rich motif (LRM2)
 CC derived from the extracellular domains of the human tyrosine kinase
 CC receptor A. The peptide constitutes the neurotrophin binding region
 CC of the receptor. The peptide may be used as an agonist of neurotrophin
 CC activity, or may be used in screening assays to identify compounds
 CC capable of binding the region critical to neurotrophin/tyrosine kinase
 CC receptor interaction, thereby acting as either antagonists or agonists
 CC of neurotrophin activity.
 XX
 XX Sequence 24 AA;
 SQ
 Query Match 100.0%; Score 21; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. NO. 93;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 DB 6 GLRF 9
 RESULT 14
 AAW36901
 ID AAW36901 standard; peptide; 24 AA.
 XX
 XX AAW36901;
 AC
 XX 01-APR-1998 (first entry)
 DT
 XX Leucine rich motif peptide of the rat tyrosine kinase receptor A.
 DE
 XX Leucine rich motif; LRM2; extracellular domain;
 KW tyrosine kinase receptor A; neurotrophin binding region;
 KW neurotrophin activity agonist; neurotrophin activity antagonist.
 XX
 OS Rattus sp.
 XX
 XX US5688911-A.
 PN
 XX

PD 18-NOV-1997.
 XX
 PF 03-MAY-1995; 95US-0434198.
 XX
 XX 03-MAY-1995; 95US-0434198.
 PR
 XX (SCHN/) SCHNEIDER R.
 PA (WIND/) WINDISCH J M.
 XX
 XX Schneider R, Windisch JM;
 PI
 XX WPI; 1998-008037/01.
 DR
 XX Tyrosine kinase receptor peptide(s) - useful in screening assays for
 PT neurotrophin agonists and antagonists
 PS Claim 1; Column 13; 8pp; English.
 XX
 CC The present sequence represents a novel leucine rich motif (LRM2)
 CC derived from the extracellular domains of the rat tyrosine kinase
 CC receptor A. The peptide constitutes the neurotrophin binding region
 CC of the receptor. The peptide may be used as an agonist of neurotrophin
 CC activity, or may be used in screening assays to identify compounds
 CC capable of binding the region critical to neurotrophin/tyrosine kinase
 CC receptor interaction, thereby acting as either antagonists or agonists
 CC of neurotrophin activity.
 XX
 XX Sequence 24 AA;
 SQ
 Query Match 100.0%; Score 21; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. NO. 93;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 DB 6 GLRF 9
 RESULT 15
 AAW40518
 ID AAW40518 standard; protein; 25 AA.
 XX
 XX AAW40518;
 AC
 XX 15-JUL-1998 (first entry)
 DT
 XX Human TrkA leucine rich motif LRM-2A fragment.
 DE
 XX Nerve growth factor; NGF; optical structure; active conformation;
 KW variable basis Monte Carlo, stimulated annealing; VBMC; ligand;
 KW neurotrophin; agonist; inhibitor; TrkA; TrkB; TrkC; NT3; p75NTR;
 KW brain-derived neurotrophic factor; human.
 XX
 OS Homo sapiens.
 OS
 XX WO9806048-A2.
 PN
 XX 12-FEB-1998.
 PD
 XX 31-JUL-1997; 97WO-CA00539.
 PF
 XX 31-JUL-1996; 96GB-0016105.
 PR
 XX (TOOH) UNIV QUEENS KINGSTON.
 PA
 XX Riopelle RJ, Ross GM, Shamovsky IL, Weaver DF;
 XX WPI; 1998-145797/13.
 DR
 XX Identifying optimal molecular structures by variable basis Monte
 PT Carlo method - particularly to determine biologically active
 PT conformation(s) of neurotrophin domains involved in receptor binding
 PT and subsequent evolution of active ligands

xx

PS Disclosure; Fig 14; 170pp; English.

xx

CC Protein fragments AAW40504-W40523 are used in a variable basis Monte
 CC Carlo (VBM) stimulated annealing method for identifying an optimal
 CC molecular structure. The method is used to identify the biologically
 CC active conformations of peptide domains of ligands, particularly
 CC neurotrophins (NT), that bind to a receptor. Once such conformations have
 CC been identified, small molecules that either inhibit NT-binding or act
 CC as agonists of the native ligand can be developed. Specifically the
 CC method is applied to (a) nerve growth factor/TrkA; (b) brain-derived
 CC neurotrophic factor, NT3 or 4/TrkB; (c) NT3/TrkC and (d) the receptor
 CC p75NTR. The preferred ligand comprises elements with proper spatial
 CC occupancy, relative atomic positions, bond type and charge for defining
 CC a 3-dimensional configuration able to bind the 3 binding areas. TrkA
 CC includes a leucine-rich motif (LRM), amino acids 93-117, with 5 binding
 CC areas: (A) Phe105TA (hydrophobic interaction); (B) Phe111TA, Phe113TA
 CC and Thr114TA (hydrophobic interaction); (C) Asp109TA and His112TA
 CC (ionic); (D) Lys100TA (ionic) and (E) Asn95TA-Ile98TA (multiple parallel
 CC beta -strand type hydrogen bonds).

xx

SQ Sequence 25 AA;

Query Match 100.0%; Score 21; DB 19; Length 25;

Best Local Similarity 100.0%; Pred. No. 97;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4

' | | | |

Db 10 GLRF 13

Search completed: March 10, 2003, 16:56:58

Job time : 11.3103 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 22.069 seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*
- 15: sp-rvirus.*
- 16: sp-bacteriap.*
- 17: sp-archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	79.3	489	11 Q8VCX4	Q8vcx4 mus musculus
2	45	77.6	473	11 Q9D8L4	Q9d8l4 mus musculus
3	43	74.1	481	11 Q8VCV5	Q8vcv5 mus musculus
4	42	72.4	117	11 Q9QXF0	Q9qxf0 mus musculus
5	42	72.4	117	11 Q9QXE9	Q9qxe9 mus musculus
6	42	72.4	586	10 Q9SNT3	Q9snt3 oryza sativ
7	41	70.7	253	16 Q8X4Z9	Q8x4z9 escherichia
8	41	70.7	310	8 Q63625	Q63625 dalbulus eb
9	41	70.7	310	8 Q63635	Q63635 baldulus tr
10	41	70.7	310	8 Q63636	Q63636 baldulus tr
11	41	70.7	481	11 Q91WT1	Q91wt1 mus musculus
12	41	70.7	550	2 Q50266	Q50266 agrobacteri
13	40	69.0	275	4 Q96L07	Q96lu7 homo sapien
14	40	69.0	310	8 Q63624	Q63624 dalbulus ci
15	40	69.0	310	8 Q63626	Q63626 dalbulus el
16	40	69.0	310	8 Q63629	Q63629 dalbulus gu

17	40	69.0	310	8	Q63630	Q63630 dalbulus lo
18	40	69.0	372	10	P93103	P93103 chenopodium
19	40	69.0	481	11	Q91WT3	Q91wt3 mus musculus
20	40	69.0	969	17	Q28863	Q28863 archaeoglob
21	39	67.2	102	11	Q9JL79	Q9jll79 mus musculus
22	39	67.2	114	11	Q9JL81	Q9jll81 mus musculus
23	39	67.2	117	11	Q9Z1C6	Q9z1c6 mus musculus
24	39	67.2	142	10	Q8W018	Q8w018 antirrhinum
25	39	67.2	142	10	Q8W017	Q8w017 antirrhinum
26	39	67.2	170	11	Q92552	Q92552 mus musculus
27	39	67.2	260	10	Q9AXC0	Q9axc0 antirrhinum
28	39	67.2	283	8	O47571	O47571 onchocerca
29	39	67.2	310	8	Q63627	Q63627 dalbulus ge
30	39	67.2	310	8	Q63628	Q63628 dalbulus ge
31	39	67.2	310	8	Q63631	Q63631 dalbulus ma
32	39	67.2	310	8	Q63632	Q63632 dalbulus ma
33	39	67.2	310	8	Q63633	Q63633 dalbulus ma
34	39	67.2	325	16	Q99S16	Q99s16 staphylococ
35	39	67.2	484	11	Q99LA6	Q99la6 mus musculus
36	38	65.5	157	4	O95978	O95978 homo sapien
37	38	65.5	187	2	Q8RM55	Q8rm55 bacteroides
38	38	65.5	241	11	Q921A6	Q921a6 mus musculus
39	38	65.5	310	8	Q63623	Q63623 dalbulus ch
40	38	65.5	339	10	Q9LJA9	Q9lja9 arabidopsis
41	38	65.5	421	16	Q97G76	Q97g76 clostridium
42	38	65.5	434	11	Q9D359	Q9d359 mus musculus
43	38	65.5	469	11	Q8R3V9	Q8r3v9 mus musculus
44	38	65.5	488	11	Q91WR1	Q91wr1 mus musculus
45	37	63.8	119	4	Q9UL94	Q9ul94 homo sapien

ALIGNMENTS

RESULT 1

Q8VCX4 PRELIMINARY: PRT: 489 AA.
ID Q8VCX4;
AC Q8VCX4;
DC 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 53.2 kDa protein.
GN A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322; AAH18322.1;
DR MGD; MGI:2144917; A1893585.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;

Query Match 79.3%; Score 46; DB 11; Length 489;

Best Local Similarity 70.0%; Pred No. 6.3;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10

II:II:IIII

DB 45 GYTFSDYFIH 54

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018455; AAI18455.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52844C5826807143 CRC64;

Query Match 74.1%; Score 43; DB 11; Length 481;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
    |||||
Db 45 GYSFDYNIY 54

RESULT 4
Q9QXF0 PRELIMINARY; PRT; 117 AA.
ID Q9QXF0;
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR NON_TER 1
FT NON_TER 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 72.4%; Score 42; DB 11; Length 117;
Best Local Similarity 66.7%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
    ||:||||:
Db 26 GYTFTDYIM 34

RESULT 5
Q9QXE9 PRELIMINARY; PRT; 117 AA.
ID Q9QXE9;
AC Q9QXE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96443; Ig-h-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Ig; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 77.6%; Score 45; DB 11; Length 473;
Best Local Similarity 77.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
    ||:||||:
Db 45 GYTFTDYII 53

RESULT 3
Q8VCV5 PRELIMINARY; PRT; 481 AA.
ID Q8VCV5;
AC Q8VCV5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).

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AI2015
hypothetical protein asl1679 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AI2015
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuriitz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2015
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-84 <KUP>
A:Cross-references: GB:BA000019; PIDN:BA078045.1; PID:gl7135499; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl1679

Query Match 100.0%; Score 21; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db 41 GLRF 44

RESULT 13
QOEC2
hypothetical protein A-87 - Escherichia coli plasmid pBR322
C:Species: Escherichia coli
C:Date: 31-Dec-1980 #sequence_revision 15-Oct-1982 #text_change 10-Sep-1999
C:Accession: A04479
R:Sutcliffe, J.G.
Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.
A:Reference number: A90923; MUID:80002802; PMID:383387
A:Accession: A04479
A:Molecule type: DNA
A:Residues: 1-87 <SUT>
C:Genetics:
A:Genome: plasmid
A:Start codon: GTG
C:Superfamily: Escherichia coli plasmid pBR322 hypothetical 10K protein

Query Match 100.0%; Score 21; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db 18 GLRF 21

RESULT 14
A83643
hypothetical protein PA0012 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83643
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Linn,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83643
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <STO>
A:Cross-references: GB:AE004441; GB:AE004091; NID:g9945828; PIDN:AAG03402.1; GSPDB:GN001

A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0012

Query Match 100.0%; Score 21; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db 81 GLRF 84

RESULT 15
B84312
hypothetical protein Vng1590h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84312
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: B84312
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE004437; NID:gl0581072; PIDN:AAG19862.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG1590H

Query Match 100.0%; Score 21; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLRF 4
Db 10 GLRF 13

Search completed: March 10, 2003, 17:01:26
Job time : 6.34483 secs

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RESULT 7
F90697
hypothetical protein ECs0550 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: F90697
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90697
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-73 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA833973.1; PID:g13360008; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs0550

Query Match 100.0%; Score 21; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 23 GLRF 26

RESULT 8
A69010
hypothetical protein MTH1077 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69010
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: A69010
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-75 <MTH>
A:Cross-references: GB:AE000879; GB:AE000666; NID:g2622175; PIDN:AAB85566.1; PID:g262217
A:Experimental source: strain Delta H
C:Genetics:
A:Start codon: TTG

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 26 GLRF 29

RESULT 9
C36817
ORF 2 protein - human papillomavirus type 41
C:Species: human papillomavirus type 41
A:Note: host Homo sapiens (man)
C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 08-Oct-1999
C:Accession: C36817
R:Hirt, L.; Hirsch-Behnham, A.; De Villiers, E.M.
Virus Res. 18, 179-190, 1990
A:Title: Nucleotide sequence of human papillomavirus (HPV) type 41: an unusual HPV type
A:Reference number: A43550
A:Accession: C36817
A:Status: translation not shown

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A:Molecule type: DNA
A:Residues: 1-76 <HIR>
A:Cross-references: EMBL:X56147; NID:g60942; PIDN:CAA39622.1; PID:g60953

Query Match 100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 68 GLRF 71

RESULT 10
T09045
hypothetical protein F26K10.170 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C:Accession: T09045
R:Bevan, M.; Lennard, N.; Ouail, M.; Harris, B.; Hajandream, M.A.; Barrell, B.G.; Ban
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16533
A:Accession: T09045
A:Molecule type: DNA
A:Residues: 1-80 <BEV>
A:Cross-references: EMBL:AL049803; GSPDB:GN00062; ATSP:F26K10.170
A:Experimental source: cultivar Columbia; BAC clone F26K10
C:Genetics:
A:Gene: ATSP:F26K10.170
A:Map position: 4
A:Introns: 41/3

Query Match 100.0%; Score 21; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 68 GLRF 71

RESULT 11
H81188
hypothetical protein NMB0518 [imported] - Neisseria meningitidis (strain MC58 serogro
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81188
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappuoli, R.;
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: H81188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <TET>
A:Cross-references: GB:AE002408; GB:AE002098; NID:g7252740; PIDN:AAF40950.1; PID:g72
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0518

Query Match 100.0%; Score 21; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 21 GLRF 24

RESULT 12

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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AG0880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-39 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02943.1; PID:g16504193; GSPDB:GN00176
C:Genetics:
A:Gene: STY3277

Query Match 100.0%; Score 21; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 5 GLRF 8

RESULT 3
D83610
hypothetical protein PA0284 [imported] - *Pseudomonas aeruginosa* (strain PAO1)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83610
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83610
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60 <STO>
A:Cross-references: GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AAG03673.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA0284

Query Match 100.0%; Score 21; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 26 GLRF 29

RESULT 4
F75371
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75371
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75371
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <WHI>
A:Cross-references: GB:AE002007; GB:AE000513; NID:g6459402; PIDN:AAF11201.1; PID:g645940
C:Genetics:
A:Gene: DR1640
A:Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 11 GLRF 14

Query Match 100.0%; Score 21; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 8 GLRF 11

RESULT 5
E96504
protein F9C16.27 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96504
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
ansen, N.F.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <STO>
A:Cross-references: GB:AE005173; NID:g8778662; PIDN:AAF79670.1; GSPDB:GN00141
C:Genetics:
A:Gene: F9C16.27
A:Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 38 GLRF 41

RESULT 6
PX0076
acrosin-like proteinase (EC 3.4.21.-) - pig (fragments)
N:Altername names: cetyltrimethylammonium bromide-extracted sperm protease
C:Species: *Sus scrofa domestica* (domestic pig)
C:Date: 22-Apr-1995 #sequence_revision 24-Oct-1997 #text_change 07-May-1999
C:Accession: PX0076
R:Akama, K.; Terao, K.; Tanaka, Y.; Noguchi, A.; Yonezawa, N.; Nakano, M.; Tobita, T.
J. Biochem. 116, 464-470, 1994
A:Title: Purification and characterization of a novel acrosin-like enzyme from boar c
A:Reference number: PX0076; MUID:95122480; PMID:7822268
A:Accession: PX0076
A:Molecule type: protein
A:Residues: 1-73 <AKA>
A:Experimental source: epididymis; sperm
A:Note: this enzyme was reported to differ from acrosin in acid solubility, kinetic p
C:Superfamily: acrosin; trypsin homology
C:Keywords: epididymis; glycoprotein; hydrolase; serine proteinase; sperm

Query Match 100.0%; Score 21; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 11 GLRF 14

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: March 10, 2003, 16:46:26 ; Search time 4.34483 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	37	D82636	hypothetical prote
2	21	100.0	39	AG0880	hypothetical prote
3	21	100.0	60	D83610	hypothetical prote
4	21	100.0	63	F75371	hypothetical prote
5	21	100.0	71	E96504	protein F9C16.27 [
6	21	100.0	73	FX0076	acrosin-like prote
7	21	100.0	73	F90697	hypothetical prote
8	21	100.0	75	A69010	hypothetical prote
9	21	100.0	76	C36817	ORF 2 protein - hu
10	21	100.0	80	T09045	hypothetical prote
11	21	100.0	83	H81188	hypothetical prote
12	21	100.0	84	A12015	hypothetical prote
13	21	100.0	87	Q0EC2	hypothetical prote
14	21	100.0	88	A83643	hypothetical prote
15	21	100.0	89	D84312	hypothetical prote
16	21	100.0	91	T17877	hypothetical prote
17	21	100.0	91	G97130	hypothetical prote
18	21	100.0	91	G97870	O-linked GlcNAc tr
19	21	100.0	93	T51189	small zinc finger-
20	21	100.0	94	AB1084	hypothetical prote
21	21	100.0	95	AC1903	hypothetical prote
22	21	100.0	101	AC0099	probable lipoprote
23	21	100.0	107	T35634	hypothetical prote
24	21	100.0	108	AD1986	hypothetical prote
25	21	100.0	110	G70791	hypothetical prote
26	21	100.0	112	E82540	conserved hypotet
27	21	100.0	112	G70855	hypothetical prote
28	21	100.0	115	AC2020	hypothetical prote
29	21	100.0	119	JN0295	Ig heavy chain V-D

30	21	100.0	121	2	A87307	hypothetical prote
31	21	100.0	122	2	D72128	hypothetical prote
32	21	100.0	122	2	G86494	hypothetical prote
33	21	100.0	122	2	A81543	hypothetical prote
34	21	100.0	122	2	T35702	hypothetical prote
35	21	100.0	123	2	F64342	hypothetical prote
36	21	100.0	125	2	A11358	protein gp30 [Bact
37	21	100.0	127	1	VXECSE	preprotein translo
38	21	100.0	127	2	S50213	ubiquinol-cytochro
39	21	100.0	127	2	H91241	preprotein translo
40	21	100.0	127	2	E86089	preprotein translo
41	21	100.0	127	2	A10456	preprotein translo
42	21	100.0	127	2	AC0934	preprotein translo
43	21	100.0	129	2	S50142	histone H3 - Leish
44	21	100.0	129	2	D90367	hypothetical prote
45	21	100.0	129	2	F82515	conserved hypotet

ALIGNMENTS

RESULT 1

D82636
hypothetical protein XF1790 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82636
R:anonymous, the Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82636
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-37 <SIM>
A:Cross-references: GB:AE004001; GB:AE003849; NID:g9106864; PIDN:AAF84598.1; GSPDB:GN
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrier, R.
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Saw
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1790

Query Match 100.0%; Score 21; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
|
|
|
|
Db 3 GLRF 6

RESULT 2

AG0880
hypothetical protein STW3277 [imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0880
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.R.; Dowd, L.; White, N.; Farr

Ig heavy chain V region (7b4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: C37263
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-72 <GOS>
A:Cross-references: GB:M57998; NID:g195479; PIDN:AAA63336.1; PID:g195480
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 67.0%; Score 65; DB 2; Length 72;
Best Local Similarity 73.3%; Pred. No. 0.0014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
I I I I I I I I I I I
DB 13 ITPYNGGTTYNQKPK 27

RESULT 14

B37263
Ig heavy chain V region (1G3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: B37263
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: B37263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-102 <GOS>
A:Cross-references: GB:M57997; NID:g195426; PIDN:AAA63335.1; PID:g195427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 67.0%; Score 65; DB 2; Length 102;
Best Local Similarity 73.3%; Pred. No. 0.002;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
I I I I I I I I I I I
DB 43 ITPYNGGTTYNQKPK 57

RESULT 15

S55535
Ig heavy chain V region pe23 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: S55535
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
atations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <BOE>
A:Cross-references: EMBL:X82592; NID:g854310; PIDN:CAA57928.1; PID:g854311
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 67.0%; Score 65; DB 2; Length 113;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFRD 17
I I I I I I I I I I I I I I I I I
DB 50 INPNNGRTSYNQKRFOD 65

Search completed: March 10, 2003, 17:01:24
Job time : 18.4655 secs

RESULT 8

MHMS75

Ig heavy chain V region (J558) - mouse (tentative sequence)

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Mar-2000

C;Accession: A26242

R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.

Nature 283, 35-40, 1980

A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements

A;Reference number: A26242; MUID:80078170; PMID:6765983

A;Accession: A26242

A;Molecule type: protein

A;Residues: 1-117 <SCH>

A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that s

C;Comment: This protein binds dextran..

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; hybridoma; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

F;22-96/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 69.1%; Score 67; DB 1; Length 117;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16

||:| || |||||:

Db 50 DINPNGGTSYNQKFK 65

RESULT 9

MHMS38

Ig heavy chain V region (AC38 205.12) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 30-May-1997

C;Accession: A02040

R;Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.

EMBO J. 3, 517-523, 1984

A;Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes

A;Reference number: A91000; MUID:84182519; PMID:6201362

A;Accession: A02040

A;Molecule type: protein

A;Residues: 1-118 <DIL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-98/Region: V segment

F;99-104/Region: D segment

F;105-118/Region: J segment

F;22-96/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 69.1%; Score 67; DB 1; Length 118;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16

||:| || |||||:

Db 50 DINPNGGTSYNQKFK 65

RESULT 10

T01407

Ig heavy chain (myeloma M104E) - mouse (fragment)

C;Species: Mus sp. (mouse)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000

C;Accession: T01407

R;Takahashi, S.; Matsuuru, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamoto

Microbiol. Immunol. 36, 855-863, 1992

A;Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and

A;Reference number: Z14317; MUID:93116638; PMID:1474935

A;Accession: T01407

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-140 <TAK>

A;Cross-references: EMBL:S51851; NID:g262657

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match

Best Local Similarity 69.1%; Score 67; DB 2; Length 140;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16

||:| || |||||:

Db 69 DINPNGGTSYNQKFK 84

RESULT 11

A49982

Ig heavy chain V region (BA7.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: A49982

R;Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleymann,

J. Biol. Chem. 269, 2805-2813, 1994

A;Title: Topology of an amiloride-binding protein.

A;Reference number: A49982; MUID:94132051; PMID:8300613

A;Accession: A49982

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <LIN>

A;Cross-references: GB:L24802; NID:g452096; PID:AAA98740.1; PID:g452097

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 68.0%; Score 66; DB 2; Length 120;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFRD 17

| |||| | ||||:

Db 51 ISPYNGATTYNQKFRD 66

RESULT 12

B47159

Ig heavy chain V region, anti-carcinoembryonic maId T84.66 antigen monoclonal anti-id

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C;Accession: B47159

R;Gaïda, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.

J. Biol. Chem. 268, 14138-14145, 1993

A;Title: Molecular characterization of a cloned idiotypic cascade containing a network

A;Reference number: A47159; MUID:93300804; PMID:7686150

A;Accession: B47159

A;Status: preliminary

A;Molecule type: DNA; protein

A;Residues: 1-136 <GAI>

A;Experimental source: hybridoma 6G6.C4

A;Note: sequence inconsistent with the nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBI:P:134422)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 68.0%; Score 66; DB 2; Length 136;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFRD 17

||||: | |||||

Db 70 IDPYDSVTHYNQKFRD 85

RESULT 13

C37263

RESULT 3

PS0057
Ig heavy chain precursor V region (PAR) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C;Accession: PS0057
R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
A;Reference number: PS0057; MUID:89197817; PMID:2467902
A;Accession: PS0057
A;Molecule type: DNA
A;Residues: 1-135 <YAO>
A;Cross-references: GB:D00307; NID:g220448; PID:BAA00213.1; PID:g220449
A;Note: The authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 71; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.00028; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2;

Qy 2 IDPYNGDTSYNQKFR 16
I:||||| I:|||||
Db 70 INPYNGDTFYNQKFK 84

RESULT 4

S26320
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S26320
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26320
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: EMBL:X59206
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 70; DB 2; Length 107;
Best Local Similarity 75.0%; Pred. No. 0.00032; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2;

Qy 2 IDPYNGDTSYNQKFRD 17
I:||||| I:||||| I:
Db 39 INPYNGATSYNQNFKD 54

RESULT 5

E45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (fra
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: E45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A;Reference number: A45722; MUID:93100833; PMID:7677958
A;Accession: E45722
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
A;Note: sequence extracted from NCBI backbone (NCBIP:120593)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 70; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 0.00036; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2;

Qy 2 IDPYNGDTSYNQKFR 16
I:||||| I:||||| I:
Db 52 INPYNGGTSYNQKFK 66

RESULT 6

S26315
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26315
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <STA>
A;Cross-references: EMBL:X59208; NID:g52079; PID:CAA41918.1; PID:g1334042
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;2-85/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 68; DB 2; Length 106;
Best Local Similarity 68.8%; Pred. No. 0.00067; Mismatches 3; Indels 0; Gaps 0;
Matches 11; Conservative 3;

Qy 2 IDPYNGDTSYNQKFRD 17
I:||||| I:||||| I:
Db 38 IDPYDSETHYNQKFKD 53

RESULT 7

MHMS4E
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 31-Mar-2000
C;Accession: A02039
R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain
A;Reference number: A02039; MUID:83075344; PMID:6816276
A;Accession: A02039
A;Molecule type: protein
A;Residues: 1-117 <KEH>
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted
F;55/Binding site: carbohydrate (Asn) (covalent) #status atypical

Query Match 69.1%; Score 67; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0011; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2;

Qy 1 DIDPYNGDTSYNQKFR 16
I:||||| I:||||| I:
Db 50 DPNPNGGTSYNQKFK 65

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 18.4655 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 IDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	73.2	98	2	SL17604
2	71	73.2	114	2	S26319
3	71	73.2	135	2	F50057
4	70	72.2	107	2	S26320
5	70	72.2	120	2	E45722
6	68	70.1	106	2	S26315
7	67	69.1	117	1	MHMS4E
8	67	69.1	117	1	MHMSJ5
9	67	69.1	118	1	MHMS38
10	67	69.1	140	2	T01407
11	66	68.0	120	2	A49882
12	66	68.0	136	2	B47159
13	65	67.0	72	2	C37263
14	65	67.0	102	2	B37263
15	65	67.0	113	2	S55535
16	64	66.0	101	2	H37262
17	64	66.0	107	2	PH0971
18	64	66.0	137	2	H32513
19	64	66.0	138	2	S45249
20	63	64.9	93	2	S42182
21	63	64.9	94	2	S42177
22	63	64.9	95	2	S42178
23	63	64.9	97	2	S42181
24	63	64.9	101	2	S42179
25	63	64.9	101	2	S42184
26	63	64.9	102	2	S42180
27	63	64.9	119	2	F30502
28	63	64.9	136	1	HVMSB1
29	62	63.9	117	1	HVMS8A

ALIGNMENTS

RESULT 1

SI17604

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: SI17604

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: SI17230; MUID:91326098; PMID:1907718

A:Accession: SI17604

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-98 <CIA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 71; DB 2; Length 98;

Best Local Similarity 80.0%; Pred. No. 0.0002;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16

Db 44 INPINGDTFYNQKFK 58

RESULT 2

S26319

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26319

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26319

A:Molecule type: mRNA

A:Residues: 1-114 <STA>

A:Cross-references: EMBL:X59172

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 71; DB 2; Length 114;

Best Local Similarity 80.0%; Pred. No. 0.00024;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16

Db 47 INPYNGDTFYNQKFK 61

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PLO231; MUID:90111618; PMID:2104919
A:Accession: PLO245
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:8-91/Domain: immunoglobulin homology <IMM>
F:24-28/Region: complementarity-determining 1
F:29-42/Region: framework 2
F:43-59/Region: complementarity-determining 2
F:60-91/Region: framework 3
F:92-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 112;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:||||:|
Db 19 GYFTDYI 27

RESULT 13
S03305
Ig heavy chain V region (6B12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C:Accession: JLO044; S05276; S03305
R:Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A:Title: Do antibodies recognize amino acid side chains of protein antigens independentl
A:Reference number: JLO043; MUID:88258372; PMID:2455014
A:Accession: JLO044
A:Molecule type: mRNA
A:Residues: 1-117 <VAN>
A:Cross-references: EMBL:X12381
R:Metzger, D.W.
submitted to the EMBL Data Library, July 1988
A:Reference number: S05276
A:Accession: S05276
A:Molecule type: mRNA
A:Residues: 1-116, 'T' <MET>
A:Cross-references: EMBL:X12381; NID:952094; PIDN:CAA30939.1; PID:g930170
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 117;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:||||:|
Db 26 GYFTDYI 34

RESULT 14
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253

C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 469;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
||:||||:|
Db 45 GYFTDYI 53

RESULT 15
S46465
Ig heavy chain V region (DA-1) - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S46465
R:Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.;
Nature Genet. 7, 162-168, 1994
A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the te
A:Reference number: S46460; MUID:95004581; PMID:7920635
A:Accession: S46465
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <COO>
A:Cross-references: EMBL:Z29977; NID:g505454; PIDN:CAA82867.1; PID:gl335176
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 75.9%; Score 44; DB 2; Length 77;
Best Local Similarity 60.0%; Pred. No. 1.2;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 10
||:||||:|
Db 14 GYFTDYMH 23

Search completed: March 10, 2003, 17:01:24
Job time : 10.8621 secs

A:Residues: 1-107 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-18/Region: framework 1
 F:3-86/Domain: immunoglobulin homology <IMM>
 F:19-23/Region: complementarity-determining 1
 F:24-37/Region: framework 2
 F:38-54/Region: complementarity-determining 2
 F:55-86/Region: framework 3
 F:87-97/Region: complementarity-determining 3
 F:98-107/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 107;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
 ||:||||:|
 Db 14 GYTFTDYI 22

RESULT 8

PH0999
 Ig heavy chain V region (clone 74-cl) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0999

R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH0999

A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-107 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 107;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
 ||:||||:|
 Db 25 GYTFTDYI 33

RESULT 9

PH0997
 Ig heavy chain V region (clone 17s-c2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0997

R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH0997

A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-109 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 109;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9

Db 26 GYTFTDYI 34
 ||:||||:|

RESULT 10

PL0244

Ig heavy chain V region (anti-DNA, Dp9VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0244

R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0244

A:Molecule type: mRNA

A:Residues: 1-110 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:8-91/Domain: immunoglobulin homology <IMM>

F:24-28/Region: complementarity-determining 1

F:29-42/Region: framework 2

F:43-59/Region: complementarity-determining 2

F:60-91/Region: framework 3

F:92-102/Region: complementarity-determining 3

F:103-110/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 110;

Best Local Similarity 77.8%; Pred. No. 1.1;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9

||:||||:|

Db 19 GYTFTDYI 27

RESULT 11

PH0998

Ig heavy chain V region (clone 165.3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0998

R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH0998

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 111;

Best Local Similarity 77.8%; Pred. No. 1.2;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9

||:||||:|

Db 26 GYTFTDYI 34

RESULT 12

PL0245

Ig heavy chain V region (anti-DNA, Dp17VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0245

R.Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
 F:132/Disulfide bonds: Interchain (to light chain) #status predicted
 F:224,227,229/Disulfide bonds: Interchain #status predicted
 F:297/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 81.0%; Score 47; DB 2; Length 446;
 Best Local Similarity 70.0%; Pred. No. 2;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
 ||:||||:|
 Db 26 GYTFTDYVIH 35

RESULT 3
 PL0242

Ig heavy chain V region (anti-DNA, S54VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0242
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0242

A:Molecule type: mRNA
 A:Residues: 1-91 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-8/Region: framework 1
 F:9-13/Region: complementarity-determining 1
 F:14-27/Region: framework 2
 F:28-44/Region: complementarity-determining 2
 F:45-76/Region: framework 3
 F:77-87/Region: complementarity-determining 3
 F:88-91/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 91;
 Best Local Similarity 77.8%; Pred. No. 0.96;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
 ||:||||:|
 Db 4 GYTFTDYVI 12

RESULT 4
 PH1165

Ig heavy chain V region (clone 26F.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1165
 R:Schitteck, B.; Rajewsky, K.
 J. Exp. Med. 176, 427-438, 1992
 A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
 A:Reference number: PH1105; MUID:92364545; PMID:1500855
 A:Accession: PH1165

A:Molecule type: DNA
 A:Residues: 1-96 <SCH>
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-96/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 96;
 Best Local Similarity 77.8%; Pred. No. 1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
 ||:||||:|
 Db 26 GYTFTDYVI 34

RESULT 5
 H47624

Ig heavy chain V-IX region - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
 C:Accession: H47624
 R:Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
 J. Exp. Med. 171, 1721-1737, 1990
 A:Title: Eleven distinct V-H gene families and additional patterns of sequence variat
 A:Reference number: H47624; MUID:90237760; PMID:2110243
 A:Accession: H47624

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-98 <HAI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 98;
 Best Local Similarity 70.0%; Pred. No. 1;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
 ||:||||:|
 Db 26 GYTFTDYWIH 35

RESULT 6
 PL0240

Ig heavy chain V region (anti-DNA, S57VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0240
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0240

A:Molecule type: mRNA
 A:Residues: 1-107 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-18/Region: framework 1
 F:19-23/Region: complementarity-determining 1
 F:24-37/Region: framework 2
 F:38-54/Region: complementarity-determining 2
 F:55-86/Region: framework 3
 F:87-97/Region: complementarity-determining 3
 F:98-107/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 107;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
 ||:||||:|
 Db 14 GYTFTDYVI 22

RESULT 7
 PL0243

Ig heavy chain V region (anti-DNA, S7VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0243
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0243

A:Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 10.8621 Seconds
(without alignments)
88.505 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	81.0	245	2 S38950	Ig gamma chain - m
2	47	81.0	446	2 S40295	Ig gamma-2a chain
3	45	77.6	91	2 PL0242	Ig heavy chain V r
4	45	77.6	96	2 PH1165	Ig heavy chain V r
5	45	77.6	98	2 H47624	Ig heavy chain V-I
6	45	77.6	107	2 PL0240	Ig heavy chain V r
7	45	77.6	107	2 PL0243	Ig heavy chain V r
8	45	77.6	107	2 PH0999	Ig heavy chain V r
9	45	77.6	109	2 PH0997	Ig heavy chain V r
10	45	77.6	110	2 PL0244	Ig heavy chain V r
11	45	77.6	111	2 PH0998	Ig heavy chain V r
12	45	77.6	112	2 PL0245	Ig heavy chain V r
13	45	77.6	117	2 S03305	Ig heavy chain V r
14	45	77.6	469	2 S74835	Ig gamma-2a chain
15	44	75.9	77	2 S46465	Ig heavy chain V r
16	44	75.9	98	2 S26909	Ig heavy chain V r
17	44	75.9	110	2 PH1000	Ig heavy chain V r
18	44	75.9	288	2 S29690	Ig heavy chain VDJ
19	43	74.1	56	2 S36386	Ig heavy chain V r
20	43	74.1	101	2 S26314	Ig heavy chain V r
21	43	74.1	105	2 S67941	Ig heavy chain var
22	43	74.1	107	2 PL0241	Ig heavy chain V r
23	43	74.1	120	2 A49982	Ig heavy chain V r
24	42	72.4	102	2 PH1235	Ig heavy chain V r
25	42	72.4	106	2 PH1002	Ig heavy chain V r
26	42	72.4	108	2 PH0977	Ig heavy chain V r
27	42	72.4	108	2 PH0975	Ig heavy chain V r
28	42	72.4	109	2 PH0973	Ig heavy chain V r
29	42	72.4	109	2 PH1001	Ig heavy chain V r

30	42	72.4	112	2 S09957	Ig heavy chain V-D
31	42	72.4	113	2 PH0974	Ig heavy chain V r
32	42	72.4	117	1 MHMS4E	Ig heavy chain V r
33	42	72.4	117	1 MHMSJ5	Ig heavy chain V r
34	42	72.4	117	2 S09960	Ig heavy chain V-D
35	42	72.4	118	1 MHMS38	Ig heavy chain V r
36	42	72.4	120	2 S19963	Ig heavy chain V r
37	42	72.4	126	2 S16280	Ig heavy chain (38
38	42	72.4	139	2 PH1225	Ig heavy chain pre
39	42	72.4	140	2 T01407	Ig heavy chain (my
40	41	70.7	36	2 S33401	Ig heavy chain V r
41	41	70.7	98	1 HVMS96	Ig heavy chain V r
42	41	70.7	98	2 S26910	Ig heavy chain V r
43	41	70.7	98	2 S17604	Ig heavy chain V r
44	41	70.7	104	2 S26466	Ig heavy chain V r
45	41	70.7	114	2 S26319	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 47; DB 2; Length 246;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTDYFIY 10
Db 26 GYFTDYFIH 35
||:||||:|

RESULT 2
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>

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OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=20165948; PubMed=10701121;
 RA Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
 RA Confalonieri F., Curtis B., Duguet M., Erauso G., Faquy D.,
 RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
 RA Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,
 RA St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,
 RA Ragan M.A., Sensen C.W.;
 RT "Gene content and organization of a 281-kbp contig from the genome of
 the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
 RL Genome 43:116-136(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726;
 RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 CC -!- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O = N-carbamoyl-L-
 aspartate.
 CC -!- COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH
 IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO
 TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY
 SIMILARITY).
 CC -!- PATHWAY: Pyrimidine biosynthesis; third step.
 CC -!- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 2.
 CC -----
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 CC -----
 DR EMBL; Y18930; CAB57689.1; ..
 DR EMBL; AE006690; AAK40922.1; ..
 DR InterPro; IPR002195; Dihydroorotase.
 DR Pfam; PF00744; Dihydroorotase; 1.
 DR PROSITE; PS00482; DIHYDROOROTASE_1; FALSE_NEG.
 DR PROSITE; PS00483; DIHYDROOROTASE_2; FALSE_NEG.
 KW Pyrimidine biosynthesis; Hydrolyase; Zinc; Complete proteome.
 FT METAL 54 54 ZINC (POTENTIAL).
 FT METAL 55 56 ZINC (POTENTIAL).
 SQ SEQUENCE 390 AA; 44332 MW; F66C94D6988E41E7 CRC64;
 Query Match 63.8%; Score 37; DB 1; Length 390;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 YSFTDYFIY 10
 || |||:|
 Db 109 YSRVDYFVY 117

Search completed: March 10, 2003, 16:57:48
 Job time : 7.2069 secs

RX MEDLINE=89128452; PubMed=2536924;
RA Lundrigan M.D., Friedrich M.J., Kadner R.J.;
RT "Nucleotide sequence of the Escherichia coli porin thermoregulatory
RL gene envy";
RN Nucleic Acids Res. 17:800-800(1989).
RC SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RC SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RC SEQUENCE FROM N.A.
RX STRAIN=K12;
RA MEDLINE=97061202; PubMed=8905232;
RA Ishima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RC -!- FUNCTION: INFLUENCE OF TEMPERATURE-DEPENDENT EXPRESSION OF SEVERAL
CC E-COLI ENVELOPE PROTEINS, MOST NOTABLY THE PORINS OMPF AND OMPG
CC AND THE LAMBDA RECEPTOR, LAMB.
CC -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC
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CC
CC EMBL: X13548; CAA31900.1; -
CC EMBL: AE000161; AAC73667.1; -
CC EMBL: U82598; AAB40763.1; -
CC EMBL: D90699; BAA35200.1; -
CC PIR: S03425; S03425.
CC EcoGene: EG10268; envy.
CC InterPro: IPR000005; HTHARAC.
CC Pfam: PF00165; HTH_Arac; 2.
CC PRINTS: PR00032; HTHARAC.
CC SMART: SM00342; HTH_ARAC; 1.
CC PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.
CC PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
KW Transcription regulation; DNA-binding; Activator; Complete proteome.
FT DNA_BIND 165 184 N-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 61 61 H -> NR (IN REF. 1).
FT CONFLICT 93 93 MISSING (IN REF. 1).
FT CONFLICT 99 99 R -> P (IN REF. 1).
FT CONFLICT 150 150 S -> T (IN REF. 1).
SQ SEQUENCE 253 AA; 29019 MW; 8FBL554CC5C4238E CRC64;

Query Match 63.8%; Score 37; DB 1; Length 253;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9

Db 1 GYSFTDY 7
27 GYDFTDY 33

RESULT 15
PYRC_SULSO
ID PYRC_SULSO STANDARD; PRT; 390 AA.
AC Q90X05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydroorotase (EC 3.5.2.3) (DHOase).
GN PYRC OR SSO0611 OR C08_039.
OS Sulfolobus solfataricus.

Db 221 GYSTSVFI 229
[[[| | | |]
RESULT 14
YAI0_ECOLI
ID YAI0_ECOLI STANDARD; PRT; 257 AA.
AC Q47534;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yai0.
GN YAI0 OR B0358.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Nashimoto H., Saito N.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RC SEQUENCE FROM N.A.
RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL: D85613; BAA12835.1; -
CC EMBL: AE000143; AAC73461.1; -
CC EMBL: U73857; AAB18083.1; -
CC EcoGene: EG13297; yai0.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 29040 MW; A6BC89571866AED8 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 257;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDY 7
27 GYDFTDY 33

RESULT 15
PYRC_SULSO
ID PYRC_SULSO STANDARD; PRT; 390 AA.
AC Q90X05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydroorotase (EC 3.5.2.3) (DHOase).
GN PYRC OR SSO0611 OR C08_039.
OS Sulfolobus solfataricus.

```

HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus.";
RL EMBO J. 7:1047-1051(1988).
CC -----
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CC -----
CC EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT NON_TER 117 117
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 63.8%; Score 37; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSTDYFYI 10
||:| |::
DB 45 GYFTGYMH 54

RESULT 12
YHIW_ECOLI
ID YHIW_ECOLI STANDARD; PRT; 242 AA.
AC P37638;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transcriptional regulator yhiw.
GN YHIW OR B3515 OR Z4928 OR ECS4395.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RL region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
RN [2]

```

```

SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [3]
SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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CC -----
CC EMBL; U00039; AAB18491.1; -;
DR EMBL; AE000428; AAC76540.1; -;
DR EMBL; AE005577; AAG58656.1; -;
DR EMBL; AP002565; BAB37818.1; -;
DR EcoGene; EGI2242; yhiw.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH_Arac; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Hypothetical protein; Transcription regulation; DNA-binding;
KW Complete proteome.
FT DNA_BIND 155 174 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 242 AA; 28028 MW; 40C11B74DA2F8DA5 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 242;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSTDYFYI 9
||| | | |
DB 211 GYSTSYFYI 219

RESULT 13
ENVY_ECOLI
ID ENVY_ECOLI STANDARD; PRT; 253 AA.
AC P10805; P77778;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Porin thermoregulatory protein envy.
GN ENVY OR B0566.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.

```

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Query Match      67.2%; Score 39; DB 1; Length 235;
Best Local Similarity 75.0%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSFDTDFI 9
DB 134 YSFNDYFV 141

RESULT 8
HV14_MOUSE
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
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CC -----
DR EMBL; J00488; AAA38519.1;
DR PIR; A02041; HVMS8A.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1
FT NON_TER 20 117 IG HEAVY CHAIN V REGION 108A.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match      65.5%; Score 38; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 7.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDY 7
DB 45 GTFTDY 51

RESULT 9
HV17_MOUSE
ID HV17_MOUSE STANDARD; PRT; 117 AA.
AC P01786;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 47A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80049769; PubMed=115869;
```

```
Robinson E.A., Appella E.;
"Amino acid sequence of a mouse myeloma immunoglobulin heavy chain
(MOPC 47 A) with a 100-residue deletion.";
J. Biol. Chem. 254:11418-11430(1979).
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE,
CC LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA
CC MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A
CC LIGHT-HEAVY CHAIN DISULFIDE BOND.
DR PIR; A02069; A1MS47.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12975 MW; 0C74BE8BB154BDF4 CRC64;

Query Match      65.5%; Score 38; DB 1; Length 117;
Best Local Similarity 55.6%; Pred. No. 7.1;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
DB 26 GTFTDYIM 34

RESULT 10
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match      65.5%; Score 38; DB 1; Length 121;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
DB 26 GTFTNYWI 34

RESULT 11
```

RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
CC -!- SIMILARITY: BELONGS TO THE ARAC/YXLS FAMILY OF TRANSCRIPTIIONAL
CC REGULATORS.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000247; AAC74572.1; -
DR EMBL: D90792; BAA15173.1; ALT_INIT.
DR EcoGene: EG13797; ydeO.
DR InterPro: IPR000005; HTHARAC.
DR Pfam: PF00165; HTH_ARAC; 2.
DR PRINTS: PR00032; HTHARAC.
DR SMART: SM00342; HTH_ARAC; 1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
DR Hypothetical protein; Transcription regulation; DNA-binding;
KW Complete proteome.
FT DNA_BIND 153 172 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 253 AA; 28725 MW; 6898BBA54DAA997 CRC64;

Query Match 70.7%; Score 41; DB 1; Length 253;
Best Local Similarity 70.0%; Pred. No. 4.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db ||:|||||
208 GYASTSYFIY 217

RESULT 6
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region BCL1 precursor.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
CC SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00494; AAA38130.1; -
DR PIR: A02042; HVMSB1.
DR HSP: P01772; 2F84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 67.2%; Score 39; DB 1; Length 136;
Best Local Similarity 60.0%; Pred. No. 5.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
Db ||:|||||
45 GVTFTDYAMH 54

RESULT 7
RNS2_ANTHI
ID RNS2_ANTHI STANDARD; PRT; 235 AA.
AC Q38716;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease S-2 precursor (EC 3.1.27.1) (Stylar glycoprotein 2)
DE (S2-RNase).
GN S2.
OS Antirrhinum hispanicum.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asterales; euasterids I; Lamiales; Veroniceae; Antirrhinum.
CC NCBI_TaxID=49039;
CC [1]
CC SEQUENCE FROM N.A.
RX TISSUE=Style;
RX MEDLINE=96240018; PubMed=8672882;
RA xue Y., Carpenter R., Dickinson H.G., Coen E.S.;
RT "Origin of allelic diversity in antirrhinum S locus RNases."
RL Plant Cell 8:805-814(1996).
CC -!- FUNCTION: SELF-INCOMPATIBILITY (SI) IS THE INHERITED ABILITY OF
CC A FLOWERING PLANT TO PREVENT SELF-FERTILIZATION BY DISCRIMINATING
CC BETWEEN SELF AND NON-SELF POLLEN DURING POLLINATION. IN MANY
CC SPECIES, SELF-INCOMPATIBILITY IS CONTROLLED BY
CC THE SINGLE, MULTIALLELIC LOCUS S.
CC -!- CATALYTIC ACTIVITY: Two-stage endonucleolytic cleavage to
CC nucleoside 3'-phosphates and 3'-phosphooligonucleotides with
CC 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: BELONGS TO THE RNASE T2 FAMILY.
CC -----
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CC -----
DR EMBL: X96465; CAA65319.1; -
DR HSP: P08056; IBOL.
DR InterPro: IPR001568; RNase_T2.
DR Pfam: PF00445; ribonuclease_T2; 1.
DR PROSITE: PS00530; RNASE_T2_1; 1.
DR PROSITE: PS00531; RNASE_T2_2; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 235 RIBONUCLEASE S-2.
FT DISULFID 80 129 BY SIMILARITY.
FT ACT_SITE 66 66 BY SIMILARITY.
FT ACT_SITE 122 122 BY SIMILARITY.
FT ACT_SITE 126 126 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 235 AA; 26767 MW; DE86ABFAEE97D7D0 CRC64;

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RN SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Cleveland B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
Db 26 GYTFDDYIM 34

RESULT 3
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFI 9
Db 26 GYTFDDYIM 34
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RESULT 4
ID HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J0501; HVMS96.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 70.7%; Score 41; DB 1; Length 98;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
Db 26 GYTFSDYIMY 35

RESULT 5
ID YDEO_ECOLI STANDARD; PRT; 253 AA.
AC P76135; P76877;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transcriptional regulator ydeO.
GN YDEO OR B1499.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshino T., Saito N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
```

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 6.2069 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-6
Perfect score: 58
Sequence: 1 GYSFTDYFIY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42	72.4	117	1 HV12_MOUSE	P01756 mus musculus
2	42	72.4	117	1 HV13_MOUSE	P01757 mus musculus
3	42	72.4	118	1 HV51_MOUSE	P06330 mus musculus
4	41	70.7	98	1 HV57_MOUSE	P18528 mus musculus
5	41	70.7	253	1 YDRO_ECOLI	P76135 escherichia
6	39	67.2	136	1 HV15_MOUSE	P01759 mus musculus
7	39	67.2	235	1 RNS2_ANTHI	Q38716 antirrhinum
8	38	65.5	117	1 HV14_MOUSE	P01758 mus musculus
9	38	65.5	117	1 HV17_MOUSE	P01786 mus musculus
10	38	65.5	121	1 HV01_MOUSE	P01745 mus musculus
11	37	63.8	117	1 HV1G_HUMAN	P23083 homo sapien
12	37	63.8	242	1 YH1W_ECOLI	P37638 escherichia
13	37	63.8	253	1 ENVY_ECOLI	P10805 escherichia
14	37	63.8	257	1 YATO_ECOLI	Q47534 escherichia
15	37	63.8	390	1 PYRC_SULSO	Q9ux05 sulfobolus
16	37	63.8	497	1 G6PI_LEGPN	Q9rdy2 legionella
17	37	63.8	519	1 CP5V_CANAP	P43083 candida api
18	37	63.8	519	1 CP5W_CANAP	Q12573 candida api
19	36	62.1	104	1 Y376_MYCGE	P47616 mycoplasma
20	36	62.1	117	1 HV04_MOUSE	P01748 mus musculus
21	36	62.1	117	1 HV06_MOUSE	P01750 mus musculus
22	36	62.1	117	1 HV09_MOUSE	P01753 mus musculus
23	36	62.1	117	1 HV10_MOUSE	P01754 mus musculus
24	36	62.1	117	1 HV49_MOUSE	P06328 mus musculus
25	36	62.1	120	1 HV1H_HUMAN	P80421 homo sapien
26	36	62.1	120	1 HV50_MOUSE	P06329 mus musculus
27	36	62.1	139	1 HV07_MOUSE	P01751 mus musculus
28	36	62.1	808	1 PHK1_ANASP	Q8yww1 anabaena sp
29	36	62.1	821	1 PHK_SYN3	P74690 synecocyst
30	35	60.3	137	1 HV11_MOUSE	P01755 mus musculus
31	35	60.3	138	1 HV48_MOUSE	P03980 mus musculus
32	35	60.3	162	1 PSFA_YERPE	Q56978 versinia pe
33	35	60.3	167	1 PSFA_YERPS	Q56981 versinia ps

ALIGNMENTS

RESULT 1

ID	HV12_MOUSE	STANDARD;	PRT;	117 AA.
AC	P01756;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ig heavy chain V region MOPC 104E.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.			
RX	MEDLINE=83075344; PubMed=6816276;			
RA	Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,			
RA	Hood L.E.;			
RT	"Complete amino acid sequence of a mouse mu chain: homology among			
RT	heavy chain constant region domains.";			
RL	Biochemistry 21:5415-5424(1982).			
CC	!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA			
CC	PROTEIN HAS ALSO BEEN DETERMINED.			
CC	!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.			
DR	PIR; A02039; MHMS4E.			
DR	HSSP; P01789; LMCP.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_v.			
DR	Pfam: PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region; Glycoprotein.			
FT	DISULFID 22 96			
FT	CARBOHYD 55 55			
FT	NON_TER 117 117			
SQ	SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE47E41 CRC64;			

Query Match 72.4%; Score 42; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTDYFI 9
DB 26 GYTFDYDM 34

RESULT 2

ID	HV13_MOUSE	STANDARD;	PRT;	117 AA.
AC	P01757;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region J558.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			


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FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 122
FT DOMAIN 123 137
FT DISULFID 41 115
FT NON_TER 137 137
SQ SEQUENCE 137 AA; ADD5881BF44B8EC9 CRC64;

Query Match 53.6%; Score 52; DB 1; Length 137;
Best Local Similarity 60.0%; Pred. No. 0.15;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFR 16
Db 70 IDPNSGGTYNEHFR 84

RESULT 14
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC -----
CC EMBL: J00536; AAA38605.1; -.
CC PIR: A02031; HVMS3.
CC HSP: P01810; 2FBJ.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; Igv; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 427C861C53975EDC CRC64;

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Query Match 52.6%; Score 51; DB 1; Length 117;
Best Local Similarity 52.9%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNOKFR 17
Db 69 NIYPSDSETHYNQKPKD 85

RESULT 15
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.;
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC PIR: A02028; HVMSG7.
CC HSP: P01789; 1MCP.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; Igv; 1.
CC Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 52.6%; Score 51; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 0.19;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNOKFR 16
Db 50 INPGNGYKYNEKFK 64

Search completed: March 10, 2003, 16:57:49
Job time : 11.5517 secs

```

DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL: J00529; AAA38170.1; -.
DR PIR: A02034; MMS18.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DISULFID 125 139 JH2 SEGMENT.
FT NON_TER 139 139 BY SIMILARITY.
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
Query Match 55.7%; Score 54; DB 1; Length 139;
Best Local Similarity 60.0%; Pred. No. 0.073;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNOKFR 16
DB 70 IDPNSGGTKYNEKFK 84
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RESULT 12
HVD6_MOUSE
ID HVD6_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL: J00539; AAA38172.1; -.
DR PIR: A02038; G2MS43.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Signal.

RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR: A02032; HVM502.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
Query Match 53.6%; Score 52; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.13;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 IDPYNGDTSYNOKFR 16
DB 70 IHPDSDDTNYNQKFK 84
|||||
RESULT 13
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
DR EMBL: J00539; AAA38172.1; -.
DR PIR: A02038; G2MS43.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Signal.

```

RN SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RL lymphocytes is encoded by a large set of antibody structural genes.";
RM EMBL J 3,517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 56.7%; Score 55; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 0.043;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPNGDTSYNOKFR 16
DB 51 INPSGGTYNEKFK 65

RESULT 9
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR EMBL; J00533; AAA38602.1; -
DR PIR; C02034; HVMS45.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 55.7%; Score 54; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.06;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPNGDTSYNOKFR 16
DB 70 IDPNSGGTYNEKFK 84

RESULT 11
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPNGDTSYNOKFR 16
DB 70 IDPNSGGTYNEKFK 84

RESULT 10
HV10_MOUSE
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 145 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR EMBL; J00533; AAA38602.1; -
DR PIR; C02034; HVMS45.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 55.7%; Score 54; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.06;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPNGDTSYNOKFR 16
DB 70 IDPNSGGTYNEKFK 84

RESULT 11
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DR EMBL; J00481; AAA38519.1; .
DR PIR; A02041; HVMS8A.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 63.9%; Score 62; DB 1; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.0031;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNOKFR 16
I I I I I I I I I I
DB 70 IYPYNGGTGYNEKFK 84

RESULT 6
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; A02030; HVMS23.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 56.7%; Score 55; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.042;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNOKFR 16
: I : I I I I I I I I I I
DB 69 NINPGNGGTNYNEKFK 84

RESULT 7
HV49_MOUSE
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----

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DR EMBL; M13788; AAA38506.1; .
DR PIR; A02035; MHMSB4.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 56.7%; Score 55; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.042;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNOKFR 16
: I I I : I I I I I I I I I I
DB 69 NIDPNSGGTKYNEKFK 84

RESULT 8
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN  SEQUENCE
RP  MEDLINE=80078170; PubMed=6765983;
RA  Schilling J., Clevinger B., Davie J.M., Hood L.;
RT  "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL  rearrangements in heavy chain V-region gene segments.";
CC  Nature 283:35-40(1980).
CC  -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC  BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC  WHICH OCCUR IN THE D AND J SEGMENTS.
CC  -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR  PIR: A26242; MHMSJ5.
DR  HSSP: P01789; IMCP.
DR  InterPro: IPR003006; Ig_MHC.
DR  InterPro: IPR003596; Ig_v.
DR  Pfam: PF00047; Ig; 1.
DR  SMART: SM00406; Igv; 1.
KW  Immunoglobulin V region.
FT  DISULFID 22 96
FT  NON_TER 117 117
SQ  SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 69.1%; Score 67; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00047;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  1 DIDPYNQDTSYNQKFR 16
Db  50 DINPNNQGTSYNQKFK 65

RESULT 3
HV51_MOUSE
ID  HV51_MOUSE STANDARD; PRT; 118 AA.
AC  P06330;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-JAN-1988 (Rel. 06, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region AC38 205.12.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=84182519; PubMed=6201362;
RA  Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT  "A V region determinant (idiotope) expressed at high frequency in B
RL  lymphocytes is encoded by a large set of antibody structural genes.";
DR  EMBO J. 3:517-523(1984).
DR  PIR: A02040; MHMS38.
DR  HSSP: P01789; IMCP.
DR  InterPro: IPR003006; Ig_MHC.
DR  InterPro: IPR003596; Ig_v.
DR  Pfam: PF00047; Ig; 1.
DR  SMART: SM00406; Igv; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 98
FT  DOMAIN 99 104
FT  DOMAIN 105 118
FT  DISULFID 22 96
FT  NON_TER 118 118
SQ  SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 69.1%; Score 67; DB 1; Length 118;
Best Local Similarity 75.0%; Pred. No. 0.00048;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  1 DIDPYNQDTSYNQKFR 16
Db  50 DINPNNQGTSYNQKFK 65

RESULT 4
HV15_MOUSE
ID  HV15_MOUSE STANDARD; PRT; 136 AA.
AC  P01759;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region BCL1 precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=82222262; PubMed=6806821;
RA  Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA  Blattner F.R.;
RT  "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT  by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RL  by two adjacent CH genes.";
RL  Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: J00494; AAA38130.1; -.
DR  PIR: A02042; HVMSB1.
DR  HSSP: P01772; 2FB4.
DR  InterPro: IPR003006; Ig_MHC.
DR  InterPro: IPR003596; Ig_v.
DR  Pfam: PF00047; Ig; 1.
DR  SMART: SM00406; Igv; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 19
FT  CHAIN 20 136
FT  NON_TER 136 136
SQ  SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 64.9%; Score 63; DB 1; Length 136;
Best Local Similarity 73.3%; Pred. No. 0.0025;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  2 IDPYNQDTSYNQKFR 16
Db  70 ISTYNGNTSYNQKFK 84

RESULT 5
HV14_MOUSE
ID  HV14_MOUSE STANDARD; PRT; 117 AA.
AC  P01758;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region 108A precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81245215; PubMed=6789211;
RA  Givoli D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT  "Diversity of germ-line immunoglobulin VH genes.";
RL  Nature 292:426-430(1981).
CC  -----
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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 10.5517 Seconds
(without alignments)
66.823 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	67	69.1	117	1 HV12_MOUSE	P01756 mus musculus
2	67	69.1	117	1 HV13_MOUSE	P01757 mus musculus
3	67	69.1	118	1 HV51_MOUSE	P06330 mus musculus
4	63	64.9	136	1 HV15_MOUSE	P01759 mus musculus
5	62	63.9	117	1 HV14_MOUSE	P01758 mus musculus
6	55	56.7	117	1 HV04_MOUSE	P01748 mus musculus
7	55	56.7	117	1 HV49_MOUSE	P06328 mus musculus
8	55	56.7	120	1 HV50_MOUSE	P06329 mus musculus
9	54	55.7	117	1 HV09_MOUSE	P01753 mus musculus
10	54	55.7	117	1 HV10_MOUSE	P01754 mus musculus
11	54	55.7	139	1 HV07_MOUSE	P01751 mus musculus
12	52	53.6	117	1 HV06_MOUSE	P01750 mus musculus
13	52	53.6	117	1 HV11_MOUSE	P01755 mus musculus
14	51	52.6	117	1 HV05_MOUSE	P01749 mus musculus
15	51	52.6	120	1 HV03_MOUSE	P01747 mus musculus
16	48	49.5	138	1 HV08_MOUSE	P03980 mus musculus
17	47	48.5	117	1 HV1B_HUMAN	P01743 homo sapien
18	46	47.4	140	1 HV02_MOUSE	P01746 mus musculus
19	46	47.4	611	1 IF4B_HUMAN	P23588 homo sapien
20	46	47.4	1302	1 RPOB_SPTCI	P47767 spiroplasma
21	45	46.4	117	1 HV52_MOUSE	P06327 mus musculus
22	44	45.4	117	1 HV1G_HUMAN	P23083 homo sapien
23	44	45.4	563	1 SVR_STRPN	Q54869 streptococ
24	43	44.3	247	1 DLX6_BRARE	Q98877 brachydanio
25	43	44.3	720	1 CAT4_HALNI	O73955 halobacteri
26	43	44.3	960	1 CSE1_YEAST	P33307 saccharomyc
27	42	43.3	503	1 HCK_RAT	P50545 rattus norv
28	42	43.3	524	1 HCK_MOUSE	P08103 mus musculus
29	41.5	42.8	183	1 USCH_HUMAN	P37286 homo sapien
30	41	42.3	508	1 GALT_BACHD	Q9Kdv2 bacillus ha
31	41	42.3	4349	1 FAT2_HUMAN	Q9nyq8 homo sapien
32	41	42.3	4351	1 FAT2_RAT	O88277 rattus norv
33	40	41.2	189	1 PMVK_DROME	Q9vit2 drosophila

34	40	41.2	211	1 HET3_RADMG	Q9u6x1 radianthus
35	40	41.2	317	1 YW91_YEAST	Q04867 saccharomyc
36	40	41.2	334	1 CHM1_MOUSE	Q921f6 mus musculus
37	40	41.2	335	1 CHM1_BOVIN	P17404 bos taurus
38	40	41.2	624	1 YH19_YEAST	P38900 saccharomyc
39	40	41.2	697	1 YHFO_YEAST	P38721 saccharomyc
40	40	41.2	805	1 YH01_TULGE	Q41608 tulipa gesn
41	40	41.2	1080	1 HDA4_CHICK	P83038 gallus gall
42	40	41.2	1374	1 YW3_YEAST	Q03099 saccharomyc
43	40	41.2	1859	1 YRF6_YEAST	P53819 saccharomyc
44	40	41.2	1876	1 GLS1_YEAST	P36331 saccharomyc
45	39.5	40.7	714	1 NCPR_CATRO	Q05001 catharanthu

ALIGNMENTS

RESULT 1
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kenry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RT Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 69.1%; Score 67; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00047;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16
Db 50 DINPNNGTSTYNQKFK 65

RESULT 2
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99028136; PubMed=9806840;
RA West A., Vojta P.J., Welch D.R., Weissman B.E.;
RT "Chromosome localization and genomic structure of the KISS-1
RL metastasis suppressor gene (KISS1).";
RL Genomics 54:145-148(1998).
RN [4]
RP ACTION ON BREAST CARCINOMA.
RX MEDLINE=97336019; PubMed=9192814;
RA Lee J.-H., Welch D.R.;
RT "Suppression of metastasis in human breast carcinoma MDA-MB-435 cells
RL after transfection with the metastasis suppressor gene, KISS-1.";
RL Cancer Res. 57:2384-2387(1997).
CC -!- FUNCTION: METASTASIS SUPPRESSOR IN MALIGNANT MELANOMA AND IN
CC SOME HUMAN BREAST CANCERS. MAY REGULATE EVENTS DOWNSTREAM OF
CC CELL-MATRIX ADHESION, PERHAPS INVOLVING CYTOSKELETAL
CC REORGANIZATION.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U43527; AAC79512.1; -.
DR Genew: HGNC:6341; KISS1.
DR MIM: 603286; -.
SQ SEQUENCE 145 AA; 15391 MW; 7B482C7436FF3BFF CRC64;

Query Match 100.0%; Score 21; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. NO. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
Db 118 GLRF 121

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Search completed: March 10, 2003, 16:57:50
 Job time : 3.48276 secs

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DE Hypothetical protein yranN.
GN YRAN OR B3148.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SIMILARITY: BELONGS TO THE UPF0102 FAMILY. STRONG, TO H. INFLUENZAE
CC H11656.
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CC -----
DR EMBL; U18997; AAA57951.1; -.
DR EMBL; AE000396; AAC76182.1; -.
DR EcoGene; EG12779; yranN
DR InterPro; IPR003509; UPF0102.
DR Pfam; PF02021; UPF0102; 1.
DR TIGRFAMs; TIGR00252; TIGR00252; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 131 AA; 14798 MW; 6A1FE67748374475 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GLRF 4
Db 35 GLRF 38
|||||

RESULT 14
CRCB_XYLFA STANDARD; PRT; 143 AA.
AC Q9PDC3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein crcb homolog.
GN CRCB OR XF1454.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=9a55c;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carver H.,
RA Coutinho L.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
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RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE CRCB FAMILY.
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CC -----
DR EMBL; AE003975; AAF84263.1; ALT_INIT.
DR InterPro; IPR003691; Camphor_CrcB.
DR Pfam; PF02537; CRCB; 1.
KW Transmembrane; Complete proteome.
FT TRANSMEM 4 26 POTENTIAL.
FT TRANSMEM 38 60 POTENTIAL.
FT TRANSMEM 75 97 POTENTIAL.
FT TRANSMEM 104 126 POTENTIAL.
SQ SEQUENCE 143 AA; 15691 MW; 325677C2FEC41580 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GLRF 4
Db 22 GLRF 25
|||||

RESULT 15
KISS_HUMAN STANDARD; PRT; 145 AA.
ID KISS1_HUMAN
AC Q15726;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Malignant melanoma metastasis-suppressor KISS-1.
GN KISS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97099426; PubMed=8944003;
RA Lee J.-H., Miele M.E., Hicks D.J., Phillips K.K., Trent J.M.,
RA Weissman B.E., Welch D.R.;
RT "KISS-1, a novel human malignant melanoma metastasis-suppressor
RT gene.";
RL J. Natl. Cancer Inst. 88:1731-1737(1996).
RN [2]
RP ERRATUM.
RA Lee J.-H., Miele M.E., Hicks D.J., Phillips K.K., Trent J.M.,
RA Weissman B.E., Welch D.R.;
RA J. Natl. Cancer Inst. 89:1549-1549(1997).
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DR StyGene; SG?????; secE.
 DR InterPro; IPR001901; SecE.
 DR InterPro; IPR004819; SecE_bac.
 DR Pfam; PF00584; SecE; 1.
 DR ProDom; PD005139; SecE_bac; 1.
 DR TIGRFAMs; TIGR00964; Sa0501s06; 1.
 DR PROSITE; PS01067; SECE_SEC61G; 1.
 KW Protein transport; Translocation; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT DOMAIN 1 18 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 19 36 PROBABLE.
 FT DOMAIN 37 44 PERIPLASMIC (PROBABLE).
 FT TRANSMEM 45 63 PROBABLE.
 FT DOMAIN 64 92 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 93 111 PROBABLE.
 FT DOMAIN 112 127 PERIPLASMIC (PROBABLE).
 SQ SEQUENCE 127 AA; 13689 MW; 640DB5C2080E775D CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 127;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 124 GLRF 127
 RESULT 11
 UCR7_KLULA
 ID UCR7_KLULA STANDARD; PRT; 127 AA.
 AC P49345; 1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ubiquinol-cytochrome C reductase complex 14 kDa protein (EC 1.10.2.2)
 DE (Complex III subunit VII).
 GN QCR7.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
 RX MEDLINE=95035106; PubMed=7948033;
 RA Mulder W., Scholten I.H., van Roon H., Grivell L.A.;
 RT "Isolation and characterisation of the linked genes APA2 and QCR7,
 RT coding for Ap4A phosphorylase II and the 14 kDa subunit VII of the
 RT mitochondrial bcl-complex in the yeast Kluyveromyces lactis.";
 RL Biochim. Biophys. Acta 1219:719-723(1994).
 CC -1- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C
 CC REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH
 CC IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN. THIS COMPONENT
 CC IS INVOLVED IN REDOX-LINKED PROTON PUMPING.
 CC -1- CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
 CC ferricytochrome c.
 CC -1- SUBUNIT: FUNGI BCL COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY
 CC SUBUNITS, 2 CORE PROTEINS AND 5 LOW-MOLECULAR WEIGHT PROTEINS (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane (Potential).
 CC -1- SIMILARITY: BELONGS TO THE UQCRB/QCR7 FAMILY.
 CC -----
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 CC -----
 CC EMBL: X76027; CAA53617.1; -
 CC InterPro: IPR003197; UCR_14kDa.
 CC Pfam; PF02271; UCR_14kDa; 1.
 KW Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
 KW Oxidoreductase.
 SQ SEQUENCE 127 AA; 14663 MW; 7195CD85B3418876 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 127;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 42 GLRF 45
 RESULT 12
 H3_LEIIN
 ID H3_LEIIN STANDARD; PRT; 129 AA.
 AC P40285;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Histone H3.
 OS Leishmania infantum.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5671;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEM 75 / Zymodeme 1;
 RX MEDLINE=95002171; PubMed=7918653;
 RA Soto M., Requena J.M., Morales G., Alonso C.;
 RT "The Leishmania infantum histone H3 possesses an extremely divergent
 RT N-terminal domain.";
 RL Biochim. Biophys. Acta 1219:533-535(1994).
 CC -1- FUNCTION: HISTONE H3, ALONG WITH HISTONE H4, PLAYS A CENTRAL ROLE
 CC IN NUCLEOSOME FORMATION.
 CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
 CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATIVELY 146 BP OF DNA.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H3 FAMILY.
 CC -----
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 CC -----
 CC EMBL: X77591; CAA54693.1; -
 CC InterPro: IPR000164; Histone_H3.
 CC InterPro; IPR004822; Histone_core.
 CC Pfam; PF00125; histone; 1.
 CC SMART; SM00428; H3; 1.
 CC PROSITE; PS00322; HISTONE_H3_1; FALSE_NEG.
 CC PROSITE; PS00959; HISTONE_H3_2; 1.
 KW Nuclear protein; Chromosomal protein; DNA-binding; Nucleosome core.
 SQ SEQUENCE 129 AA; 14629 MW; C8AB2EA73C906100 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 75 GLRF 78
 RESULT 13
 YRAN_ECOLI
 ID YRAN_ECOLI STANDARD; PRT; 131 AA.
 AC P45465;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [6]
 RN TOPOLOGY.
 RX MEDLINE=91266903; PubMed=2050112;
 RA Schatz P.J., Bieker K.L., Ottemann K.M., Silhavy T.J., Beckwith J.;
 RT "One of three transmembrane stretches is sufficient for the
 RT functioning of the SecE protein, a membrane component of the *E. coli*
 RT secretion machinery.";
 RL EMBO J. 10:1749-1757(1991).
 RN [7]
 RN SUBUNITS
 RX MEDLINE=20402345; PubMed=10944122;
 RA Yahr T.L., Wickner W.T.;
 RT "Evaluating the oligomeric state of SecYEG in preprotein
 RT translocase.";
 RL EMBO J. 19:4393-4401(2000).
 RN [8]
 RN SUBUNITS
 RX MEDLINE=20164453; PubMed=10698927;
 RA Manting E.H., van Der Does C., Remigy H., Engel A., Driessen A.J.;
 RT "SecYEG assembles into a tetramer to form the active protein
 RT translocation channel.";
 RL EMBO J. 19:852-861(2000).
 RN [9]
 RN MUTANTS
 RX MEDLINE=95196752; PubMed=7889938;
 RA Flower A.M., Osborne R.S., Silhavy T.J.;
 RT "The allele-specific synthetic lethality of *prlA*-*prlG* double mutants
 RT predicts interactive domains of SecY and SecE.";
 RL EMBO J. 14:884-893(1995).
 CC -!- FUNCTION: ESSENTIAL FOR PROTEIN EXPORT.
 CC -!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLLOCATION APPARATUS
 CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECY. THE
 CC TRANSLLOCATION CHANNEL SEEMS TO BE COMPOSED OF A SECA HOMODIMER AND
 CC FOUR COPIES OF A SECYEG COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE SECE/SEC61-GAMMA FAMILY.
 CC -----
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 CC -----
 DR EMBL; M30610; AAA24621.1; -;
 DR EMBL; U00006; AAC43079.1; -;
 DR EMBL; AE000472; AAC76955.1; -;
 DR EMBL; AE005629; AAG59177.1; -;
 DR EMBL; AP002567; BAB38327.1; -;
 DR PIR; A35139; VPECSE.
 DR PIR; S16341; S16341.
 DR EcoGene; EG10939; secE.
 DR InterPro; IPR001901; SecE.
 DR InterPro; IPR004819; SecE_bac.
 DR Pfam; PF00584; SecE; 1.
 DR ProDom; PD005139; SecE_bac; 1.
 DR TIGRFAMS; TIGR00964; 3a0501s06; 1.
 DR PROSITE; PS01067; SECE; SEC61; 1.
 KW Protein transport; Translocation; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT DOMAIN 1 18 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 19 36 PROBABLE.
 FT DOMAIN 37 44 PERIPLASMIC (PROBABLE).
 FT TRANSMEM 45 63 PROBABLE.
 FT DOMAIN 64 92 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 93 111 PROBABLE.

FT DOMAIN 112 127 PERIPLASMIC (PROBABLE).
 SQ SEQUENCE 127 AA; 13643 MW; 94D37280522875CE CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 127;
 Best Local Similarity 100.0%; Pred. NO. 87;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLRF 4
 Db 124 GLRF 127
 RESULT 10
 SECE_SALTY STANDARD; PRT; 127 AA.
 AC Q9L9KI;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Preprotein translocase secE subunit.
 GN SECE OR STM4147 OR STM41.6 OR STY3738.
 OS *Salmonella typhimurium*, and
 OS *Salmonella typhi*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Salmonella*.
 OX NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churchill J., Duggan G., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar typhi CT18";
 RL Nature 413:848-852(2001).
 CC -!- FUNCTION: ESSENTIAL FOR PROTEIN EXPORT (By similarity).
 CC -!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLLOCATION APPARATUS
 CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECY. THE
 CC TRANSLLOCATION CHANNEL SEEMS TO BE COMPOSED OF A SECA HOMODIMER AND
 CC FOUR COPIES OF A SECYEG COMPLEX (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SECE/SEC61-GAMMA FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF170176; AAF33494.1; -;
 DR EMBL; AE008893; AAL22975.1; -;
 DR EMBL; AL627279; CAD09493.1; -;

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RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierulave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geobaghen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: SOME, TO E.COLI YIHN.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; U67488; AAB98332.1; -.
DR TIGR; MJ0342; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 123 AA; 14008 MW; E2463D19323D5919 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
Db 55 GLRF 58

RESULT 8
G8_HUMAN
ID G8_HUMAN STANDARD; PRT; 126 AA.
AC Q9UBA6; Q9UBA8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE G8 protein.
GN G8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93206277; PubMed=8096093;
RA Partanen J., Milner C., Campbell R.D., Maki M., Lipsanen V.,
RA Koskimies S.;
RT "HLA-linked heat-shock protein 70 (HSP70-2) gene polymorphism and
RT celiac disease."
RL Tissue Antigens 41:15-19(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfal G., Haykett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

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CC EMBL; AJ249732; CAB56508.1; -.
DR EMBL; AJ249731; CAB56506.1; -.
DR MIM; 605447; -.
KW Alternative splicing.
FT VARSPLIC 86 126
FT SEQUENCE 126 AA; 13270 MW; 59610E786B9C4F60 CRC64;
SQ SEQUENCE 126 AA; 13270 MW; 59610E786B9C4F60 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
Db 108 GLRF 111

RESULT 9
SECE_ECOLI
ID SECE_ECOLI STANDARD; PRT; 127 AA.
AC P16920;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Preprotein translocase sece subunit.
GN SECE OR PRLG OR B3981 OR Z5554 OR EGS4904.
OS Escherichia coli, and
OS Escherichia coli, O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90170882; PubMed=2137819;
RA Downing W.L., Sullivan S.L., Gottesman M.E., Dennis P.P.;
RT "Sequence and transcriptional pattern of the essential Escherichia
RT coli sece-nusg operon."
RL J. Bacteriol. 172:1621-1627(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378734; PubMed=2673920;
RA Schatz P.J., Riggs P.D., Jacq A., Fath M.J., Beckwith J.;
RT "The sece gene encodes an integral membrane protein required for
RT protein export in Escherichia coli."
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes."
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfal G., Haykett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

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DE Mitochondrial import inner membrane translocase subunit Tim9.
GN TIM9.
OS Zygosaccharomyces baillii.
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
CC NCBI_TaxID=4954;
RN [1]
RP SEQUENCE FROM N.A.
RA Mollapour M., Piper P.W.;
RT "Targeted gene deletion in Zygosaccharomyces baillii.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -----
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CC -----
CC EMBL; AF279260; AAG17695.1; .
DR InterPro; IPR004217; Znf_Tim10/DDP.
DR Pfam; PF02953; zf-Tim10_DDP; 1.
KW Transport; Protein transport; Translocation; Mitochondrion;
KW Inner membrane.
SQ SEQUENCE 87 AA; 10198 MW; BBAB2C5D909347CD CRC64;

Query Match 100.0%; Score 21; DB 1; Length 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
DB 71 GLRF 74

RESULT 3
YPB2_ECOLI STANDARD; PRT; 87 AA.
ID YPB2_ECOLI
AC P03850;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hypothetical 10.0 kDa protein.
OS Escherichia coli.
OG Plasmid pBR322.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
CC NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=60002802; PubMed=383387;
RA Sutcliffe J.G.;
RT "Complete nucleotide sequence of the Escherichia coli plasmid
RT pBR322."
RL Cold Spring Harb. Symp. Quant. Biol. 43:77-90(1979).
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CC -----
CC EMBL; J01749; .; NOT_ANNOTATED_CDS.
DR PIR; A04479; Q0BC2.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 87 AA; 10035 MW; D665A3EAC7129D4F CRC64;

Query Match 100.0%; Score 21; DB 1; Length 87;

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Best Local Similarity 100.0%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
DB 18 GLRF 21

RESULT 4
DPM3_MOUSE STANDARD; PRT; 92 AA.
ID DPM3_MOUSE
AC Q9D1Q4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dolichol-phosphate mannosyltransferase subunit 3 (Dolichol-phosphate
DE mannosyltransferase subunit 3) (Dolichyl-phosphate beta-D-
DE mannosyltransferase subunit 3) (Mannose-P-dolichol synthase subunit 3)
DE (MPD synthase subunit 3) (DPM synthase complex subunit 3).
GN DPM3.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Stabilizer subunit of the dolichol-phosphate-mannose
CC synthase complex (By similarity).
CC -!- SUBUNIT: Composed of three subunits; DPM1, DPM2 and DPM3.
CC Associated with DPM1 via its C-terminal domain and with DPM2 via
CC its N-terminal portion (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DPM3 FAMILY.
CC -----
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CC -----
CC EMBL; AK003223; BAB22652.1; .
DR MGD; MG1:1915813; I110001H19Rik.
KW Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 37 57 POTENTIAL.
SQ SEQUENCE 92 AA; 10139 MW; B621E6E47337CC40 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 92;

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RESULT 2			
IM09_ZYGBA	IM09_ZYGBA	STANDARD;	PRT; 87 AA.
ID	IM09_ZYGBA		
AC	P57745		
DT	16-OCT-2001	(Rel. 40; Created	
DT	16-OCT-2001	(Rel. 40; Last sequence update)	
DT	16-OCT-2001	(Rel. 40; Last annotation update)	

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RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vanathavan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Kechum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE002007; AAF11201.1; -;
DR TIGR; DR1640; -;
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 63 AA; 6982 MW; 116456AA28DD5BD CRC64;

Query Match 100.0%; Score 21; DB 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
Db 8 GLRF 11

RESULT 14
Q8S140
ID Q8S140 PRELIMINARY; PRT; 70 AA.
AC Q8S140;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P0415A04.1 protein.
GN P0415A04.1.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
RT clone:P0415A04.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003345; BAB90093.1; -;
SQ SEQUENCE 70 AA; 8046 MW; 761A5B711F5663B5 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
Db 22 GLRF 25

RESULT 15
Q9LNZ1
ID Q9LNZ1 PRELIMINARY; PRT; 71 AA.
AC Q9LNZ1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE F9C16.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kieleczawa J., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,

RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
RA Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F9C16 from chromosome
RT I.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC022314; AAF79670.1; -;
SQ SEQUENCE 71 AA; 8435 MW; 8AD3B9A8924B1E2A CRC64;

Query Match 100.0%; Score 21; DB 10; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
Db 38 GLRF 41

Search completed: March 10, 2003, 17:00:14
Job time : 10.8276 secs

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SBW25;
 RA Preston G.M., Bertrand N., Rainey P.B.;
 RT "Type III secretion in plant growth-promoting Pseudomonas fluorescens
 RT SBW25.";
 RL Mol. Microbiol. 0:0-0(2001).
 DR EMBL: AY038582; AAK74144.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 58 AA; 6584 MW; 312FA3FC60385E4D CRC64;

Query Match 100.0%; Score 21; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 7 GLRF 10

RESULT 10

O8VX80 PRELIMINARY; PRT; 58 AA.

AC Q8VX80;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Hypothetical 6.4 kDa protein (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ROOT;
 RA Dubos C., Plomion C.;

RT "Identification of water-deficit responsive genes in maritime pine
 RT (Pinus pinaster Ait.) roots using non radioactive cDNA-AFLP.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ300727; CAC83311.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 FT 58
 SQ SEQUENCE 58 AA; 6392 MW; ACC433733EE41A7 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 58;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 46 GLRF 49

RESULT 11

O90VY6 PRELIMINARY; PRT; 59 AA.

AC O90VY6;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Survivin gamma (Survivin short).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Langer J.S., Bridgham J.T., Johnson A.L.;

RT "Molecular cloning and characterization of novel chicken survivin
 RT splicing variants.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF377324; AAK56309.1; -.
 DR EMBL: AF377322; AAK56307.1; -.
 SQ SEQUENCE 59 AA; 6716 MW; 79FE9B7DA6C2A2CA CRC64;

Query Match 100.0%; Score 21; DB 13; Length 59;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 48 GLRF 51

RESULT 12

O916K6 PRELIMINARY; PRT; 60 AA.

AC Q916K6;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE Hypothetical protein PA0284.
 GN PA0284.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 RL EMBL: AE004466; AAG03673.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 60 AA; 6733 MW; 5F0889358D97FA57 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4

Db 26 GLRF 29

RESULT 13

O9RTW3 PRELIMINARY; PRT; 63 AA.

AC O9RTW3;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 GN DRI640.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.;

```
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Heque A., Hien T.T., Holroyd S., Jegels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627277; CAP02943.1; -.
DR InterPro; IPR001230; Prenyl_site.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 39 AA; 4450 MW; CF0A930C832A41B3 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 5 GLRF 8

RESULT 6
Q8VJM3 ID Q8VJM3 PRELIMINARY; PRT; 41 AA.
AC Q8VJM3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein MT2369.
GN MT2369.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE007078; AAK46659.1; -.
DR TIGR; MT2369; -.
KW Hypothetical protein.
SQ SEQUENCE 41 AA; 4309 MW; 9F71B43DB6955C92 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 23 GLRF 26

RESULT 7
Q9IX54 ID Q9IX54 PRELIMINARY; PRT; 42 AA.
AC Q9IX54;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Major core protein (Fragment).
OS Possum adenovirus.

RA Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Adenovirus.
OX NCBI_TaxID=121816;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomson D.M., Meers J.;
RT "Molecular confirmation of an adenovirus in brushtail possums
RT (Trichosurus vulpecula).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249333; AAF65557.1; -.
DR InterPro; IPR004912; Adeno_VII.
DR Pfam; PF03228; Adeno_VII; 1.
FT NON_TER 42
SQ SEQUENCE 42 AA; 4765 MW; 87C1D4978D1D13EC CRC64;

Query Match 100.0%; Score 21; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 25 GLRF 28

RESULT 8
Q93VA2 ID Q93VA2 PRELIMINARY; PRT; 56 AA.
AC Q93VA2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P0487H02.23 protein (P0682B08.4 protein).
GN P0487H02.23 OR P0682B08.4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0487H02.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0682B08.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002883; BAB67863.1; -.
DR EMBL; AP003578; BAB60934.1; -.
SQ SEQUENCE 56 AA; 6501 MW; DED2A3D88ACF4C60 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRF 4
Db 42 GLRF 45

RESULT 9
Q8VPK5 ID Q8VPK5 PRELIMINARY; PRT; 58 AA.
AC Q8VPK5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 6.6 kDa protein.
OS Pseudomonas fluorescens.
```

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Elongation factor EF-Tu (Fragment).
GN TUFA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99429862; PubMed=10498727;
RA Allen T., Shen P., Samsel L., Liu R., Lindahl L., Zengel J.M.;
RT "Phylogenetic analysis of L4-mediated autogenous control of the S10
ribosomal protein operon";
RL J. Bacteriol. 181:6124-6132(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Noorani S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF058451; AAC14291.1;
DR InterPro: IPR004160; EFTU_Cterm.
DR Pfam: PF03143; GTP_EFTU_D3; 1.
FT NON_TER
SQ SEQUENCE 26 AA; 2659 MW; 979F0015618DE7EB CRC64;
Query Match 100.0%; Score 21; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. NO. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLRF 4
Db 4 GLRF 7
RESULT 3
Q8VJT7 PRELIMINARY; PRT; 35 AA.
AC Q8VJT7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein MT2011.
GN MT2011.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE007054; AAK46283.1;
DR TIGR: MT2011;
KW Hypothetical protein.
SQ SEQUENCE 35 AA; 3901 MW; F9ED2D87A4F808F CRC64;
Query Match 100.0%; Score 21; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLRF 4
Db 7 GLRF 10
RESULT 4
Q9PCI9

ID Q9PCI9 PRELIMINARY; PRT; 37 AA.
AC Q9PCI9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Xfi1790.
GN Xfi1790.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=9A5C;
MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arraya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Bueno M.R.P., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.B., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lenos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.B.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.P., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL: AE004001; AAF84598.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 37 AA; 3952 MW; D2656E66BA48E9E CRC64;
Query Match 100.0%; Score 21; DB 16; Length 37;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLRF 4
Db 3 GLRF 6
RESULT 5
Q8Z3T7 PRELIMINARY; PRT; 39 AA.
ID Q8Z3T7
AC Q8Z3T7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SPY3277.
GN SPY3277
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;

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OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 8.82759 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-8
Perfect score: 21
Sequence: 1 GLRF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_protist.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	100.0	26	2	O68929
2	21	100.0	26	2	O68933
3	21	100.0	35	16	O8VJT7
4	21	100.0	37	16	O9PC19
5	21	100.0	39	16	O8Z3T7
6	21	100.0	41	16	O8VJM3
7	21	100.0	42	12	O9IX54
8	21	100.0	56	10	O93VA2
9	21	100.0	58	2	O8VPK5
10	21	100.0	58	10	O8VX80
11	21	100.0	59	13	O90VY6
12	21	100.0	60	16	O9I6K6
13	21	100.0	63	16	O9RTW3
14	21	100.0	70	10	O8SI40
15	21	100.0	71	10	O9LNZ1
16	21	100.0	73	2	O8RPP0

17	21	100.0	73	16	O988N8	Q988n8 rhizobium l
18	21	100.0	73	16	O8X2S9	Q8x2s9 escherichia
19	21	100.0	75	17	O27149	Q27149 methanobact
20	21	100.0	76	12	O84214	Q84214 human papil
21	21	100.0	77	16	O92MC1	Q92mc1 rhizobium m
22	21	100.0	79	5	O8T948	Q8t948 drosophila
23	21	100.0	80	10	O9M0H9	Q9m0h9 arabidopsis
24	21	100.0	83	1	O8X2S3	Q8x2s3 halobacteri
25	21	100.0	83	16	O9K0R2	Q9k0r2 neisseria m
26	21	100.0	84	16	O9YWD4	Q9ywd4 anabaena sp
27	21	100.0	85	2	O8YAM7	Q8yam7 salmonella
28	21	100.0	86	2	O936F6	Q936f6 staphylococ
29	21	100.0	88	5	O27405	Q27405 pratylenchu
30	21	100.0	88	16	O9I7B4	Q9i7b4 pseudomonas
31	21	100.0	89	17	O9HPK5	Q9hpk5 halobacteri
32	21	100.0	90	4	O9UBV1	Q9ubv1 homo sapien
33	21	100.0	91	12	O984Z9	Q984z9 paramecium
34	21	100.0	91	16	O97HV6	Q97hv6 clostridium
35	21	100.0	91	16	O92FW0	Q92fw0 rickettsia
36	21	100.0	94	16	O8YAP4	O8yap4 listeria mo
37	21	100.0	95	16	O8YFS3	Q8yfs3 anabaena sp
38	21	100.0	97	10	O9LRT6	Q9lrt6 arabidopsis
39	21	100.0	97	17	O8TRU8	Q8tru8 methanosarc
40	21	100.0	98	6	O95N84	Q95n84 ovis aries
41	21	100.0	99	2	O93DW6	Q93dw6 mycoplasma
42	21	100.0	99	10	O8SAW8	O8saw8 oryza sativ
43	21	100.0	99	17	O9HL46	Q9hl46 thermoplas
44	21	100.0	100	16	O98FX9	Q98fx9 rhizobium l
45	21	100.0	101	16	O8ZHS9	Q8zhs9 yersinia pe

ALIGNMENTS

RESULT 1

O68929 ID O68929 PRELIMINARY; PRT; 26 AA.
AC O68929;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Elongation factor EF-Tu (Fragment).
GN TUFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR30;
RA Noorani S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF058450; AAC14286.1; -
DR InterPro; IPR004160; EFTU.Cterm.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 2645 MW; 92387015618DE7EB CRC64;

Query Match 100.0%; Score 21; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRF 4
| | | |
Db 4 GLRF 7

RESULT 2

O68933 ID O68933 PRELIMINARY; PRT; 26 AA.
AC O68933;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

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ID Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GS V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069913; BAB63929.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 57.7%; Score 56; DB 11; Length 142;
Best Local Similarity 56.2%; Pred. No. 0.18;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
:|:| | | | | | | |
DB 50 NINPSNGGTNYNEKFR 65

RESULT 14
Q921C4
ID Q921C4 PRELIMINARY; PRT; 118 AA.
AC Q921C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/g4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR HSPF; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 56.7%; Score 55; DB 11; Length 118;
Best Local Similarity 73.3%; Pred. No. 0.21;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
| | :| | | | | | |
DB 51 IYPGDGDTSYTQKFR 65

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RESULT 15

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Q925S2
ID Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 56.7%; Score 55; DB 11; Length 170;
Best Local Similarity 60.0%; Pred. No. 0.32;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNQKFR 16
| | :| | | | | | |
DB 53 ISTDGNINYNQKFR 67

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Search completed: March 10, 2003, 17:00:12

Job time : 37.5172 secs

RC TISSUE-COLON;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013488; AAH13488.1; -
 DR MGD; MGI:2144917; AJ893585;
 DR InterPro; IPR003598; Ig_C2;
 DR Pfam; PF00047; Ig_4;
 DR SMART; SM00408; IGC2; 1;
 DR PROSITE; PS00290; IGC_MHC; UNKNOWN_2;
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 481 AA; 52022 MW; 4EB5C253038B718 CRC64;
 Query Match 59.8%; Score 58; DB 11; Length 481;
 Best Local Similarity 66.7%; Pred. No. 0.36;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IDPYNGDTSYNOKFR 16
 DB 70 IDPFDSTSYNOKFK 84
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RESULT 10
 Q9JL75 PRELIMINARY; PRT; 109 AA.
 AC Q9JL75;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206031; AAF69329.1; -
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1;
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;
 Query Match 57.7%; Score 56; DB 11; Length 109;
 Best Local Similarity 60.0%; Pred. No. 0.13;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPYNGDTSYNOKFR 16
 DB 42 INPYNDGTYNEKFK 56
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 RESULT 11
 Q9GY22 PRELIMINARY; PRT; 119 AA.
 AC Q9GY22;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
 DE (Fragment).
 OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 variable region gene of monoclonal anti-idiotypic antibody NP30 of
 Schistosoma japonicum";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282622; AAG01452.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1;
 DR PRINTS; PR01573; SUPERTUBBY.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00410; IG_like; 1.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;
 Query Match 57.7%; Score 56; DB 5; Length 119;
 Best Local Similarity 62.5%; Pred. No. 0.15;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IDPYNGDTSYNOKFRD 17
 DB 51 INPSRGTYNOKFKD 66
 ||:| |::|||::|
 ||:| |::|||::|
 RESULT 12
 Q924P8 PRELIMINARY; PRT; 140 AA.
 AC Q924P8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE V23-D-J-C mu protein (Fragment).
 GN V23-D-J-C MU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB069917; BAB63933.1; -
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1;
 FT NON_TER 1
 FT NON_TER 140
 SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;
 Query Match 57.7%; Score 56; DB 11; Length 140;
 Best Local Similarity 56.2%; Pred. No. 0.18;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIDPYNGDTSYNOKFR 16
 DB 50 NINPSNGGTNYNEKFK 65
 :||: |||::||:
 :||: |||::||:
 RESULT 13
 Q924Q1

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Anti-DNA heavy chain (Fragment).
 GN J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HEJ-LPR/LPR;
 RX MEDLINE=96409289; PubMed=8814271;
 RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among
 anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
 RL Eur. J. Immunol. 26:2225-2233(1996).
 DR EMBL: U59154; AA02916.1; -.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 123
 SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;
 Query Match 66.0%; Score 64; DB 11; Length 123;
 Best Local Similarity 64.7%; Pred. No. 0.0074;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DIDPYNGDTSYNOKFRD 17
 DB 50 DINPYGGTRYSQKFXD 66
 RESULT 7
 Q96GA6
 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
 AC Q96GA6;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Unknown (protein for MGC:15420).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-CELL;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC009851; AAH09851.1; -.
 DR InterPro: IPR000005; HTHARAC.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00408; IGC2; 2.
 DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
 Query Match 61.9%; Score 60; DB 4; Length 614;
 Best Local Similarity 62.5%; Pred. No. 0.22;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IDPYNGDTSYNOKFRD 17
 DB 70 ITPFNGNTNVAQKFD 85
 RESULT 8

Q9DCD9
 ID Q9DCD9 PRELIMINARY; PRT; 426 AA.
 AC Q9DCD9;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Adult male kidney cDNA, RIKEN full-length enriched library,
 clone:0610041A01, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee-N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK002875; BAB22422.1; -.
 DR HSP: P01810; 2FEJ.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; Ig; 3.
 DR SMART: SM00407; IGC1; 3.
 DR SMART: SM00410; IG_like; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 426 AA; 45819 MW; 56E1275BA48F6FB1 CRC64;
 Query Match 59.8%; Score 58; DB 11; Length 426;
 Best Local Similarity 90.9%; Pred. No. 0.31;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 NGDTSYNOKFR 16
 DB 17 NGDTSYNOKFK 27
 RESULT 9
 Q91WT3
 ID Q91WT3 PRELIMINARY; PRT; 481 AA.
 AC Q91WT3;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical 52.0 kDa protein.
 GN AI893585.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.


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DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018455; AAI18455.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 73.2%; Score 71; DB 11; Length 481;
Best Local Similarity 80.0%; Pred. No. 0.0026;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDPYNGDTSYNQKFR 16
Db 70 IDPYNGGSSYNQKFK 84

RESULT 3
Q920E8 PRELIMINARY; PRT; 120 AA.
ID Q920E8
AC Q920E8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307936; AAL09420.1; -
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF00047; Ig; 1.
DR NON_TER 1
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 70.1%; Score 68; DB 11; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.0016;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16
Db 50 NIDPYGGSYNQKFK 65

RESULT 4
Q9QXF0 PRELIMINARY; PRT; 117 AA.
ID Q9QXF0
AC Q9QXF0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
```

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AC Q9QXF0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 69.1%; Score 67; DB 11; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16
Db 50 DINPNNGGTSYNQKFK 65

RESULT 5
Q9QXE9 PRELIMINARY; PRT; 117 AA.
ID Q9QXE9
AC Q9QXE9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 69.1%; Score 67; DB 11; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIDPYNGDTSYNQKFR 16
Db 50 DINPNNGGTSYNQKFK 65

RESULT 6
Q8VIL1 PRELIMINARY; PRT; 123 AA.
ID Q8VIL1
AC Q8VIL1;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 16:46:26 ; Search time 37.5172 Seconds
(without alignments)
93.365 Million cell updates/sec

Title: US-09-924-099-7
Perfect score: 97
Sequence: 1 DIDPYNGDTSYNQKFRD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	76	78.4	488	11 Q91WR1	Q91wr1 mus musculus
2	71	73.2	481	11 Q8VCV5	Q8vcv5 mus musculus
3	68	70.1	120	11 Q920E8	Q920e8 mus musculus
4	67	69.1	117	11 Q9QXF0	Q9qxf0 mus musculus
5	67	69.1	117	11 Q9QXE9	Q9qxe9 mus musculus
6	64	66.0	123	11 Q8VIJ1	Q8vij1 mus musculus
7	60	61.9	614	4 Q96GA6	Q96ga6 homo sapien
8	58	59.8	426	11 Q9DCD9	Q9dcd9 mus musculus
9	58	59.8	481	11 Q91WT3	Q91wt3 mus musculus
10	56	57.7	109	11 Q9JL75	Q9jl75 mus musculus
11	56	57.7	119	5 Q9GYZ2	Q9gyz2 schistosoma
12	56	57.7	140	11 Q924P8	Q924p8 mus musculus
13	56	57.7	142	11 Q924Q1	Q924q1 mus musculus
14	55	56.7	118	11 Q921C4	Q921c4 mus musculus
15	55	56.7	170	11 Q925S2	Q925s2 mus musculus
16	54	55.7	137	11 Q924R6	Q924r6 mus musculus

17	54	55.7	139	11	Q924R5	Q924r5 mus musculus
18	54	55.7	140	11	Q924R2	Q924r2 mus musculus
19	54	55.7	141	11	Q924Q4	Q924q4 mus musculus
20	54	55.7	143	11	Q924R7	Q924r7 mus musculus
21	54	55.7	143	11	Q924R0	Q924r0 mus musculus
22	54	55.7	143	11	Q924O5	Q924o5 mus musculus
23	54	55.7	143	11	Q91VA2	Q91va2 mus musculus
24	54	55.7	144	11	Q924P5	Q924p5 mus musculus
25	54	55.7	144	11	Q924R4	Q924r4 mus musculus
26	54	55.7	145	11	Q924R3	Q924r3 mus musculus
27	54	55.7	145	11	Q924R1	Q924r1 mus musculus
28	54	55.7	145	11	Q924O9	Q924o9 mus musculus
29	54	55.7	145	11	Q924O7	Q924o7 mus musculus
30	54	55.7	145	11	Q924O6	Q924o6 mus musculus
31	54	55.7	145	11	Q924P7	Q924p7 mus musculus
32	54	55.7	146	11	Q924R8	Q924r8 mus musculus
33	54	55.7	146	11	Q924Q8	Q924q8 mus musculus
34	54	55.7	146	11	Q924Q3	Q924q3 mus musculus
35	52	53.6	143	11	Q924O0	Q924o0 mus musculus
36	52	53.6	143	11	Q924P9	Q924p9 mus musculus
37	52	53.6	278	11	Q921K1	Q921k1 mus musculus
38	51	52.6	114	11	Q9JL81	Q9jl81 mus musculus
39	51	52.6	468	11	Q99L31	Q99l31 mus musculus
40	50	51.5	110	11	Q9JL77	Q9jl77 mus musculus
41	50	51.5	119	9	Q8SDV7	Q8sdv7 bacterioph
42	50	51.5	123	16	Q931Z9	Q931z9 staphylococ
43	50	51.5	143	11	Q91V67	Q91v67 mus musculus
44	48	49.5	111	11	Q9D9B8	Q9d9b8 mus musculus
45	47	48.5	124	4	Q9UL92	Q9ul92 homo sapien

ALIGNMENTS

RESULT 1

Q91WR1 PRELIMINARY; PRT; 488 AA.
ID Q91WR1
AC Q91WR1
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 53.0 kDa protein.
GN A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC013539; AAI893585.
DR MGI; MGI:2144917; A1893585.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 78.4%; Score 76; DB 11; Length 488;
Best Local Similarity 81.2%; Pred. No. 0.00041;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIDPYNGDTSYNQKFR 16
||:|||||
Db 69 DINPYNGGTSYNQKFK 84

RESULT 2

Q8VCV5 PRELIMINARY; PRT; 481 AA.
ID Q8VCV5
AC Q8VCV5;

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RT "Octopine-type Ti plasmid sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF242881; AAB88471.1; -;
 DR InterPro: IPR003692; Hydantoinase_B.
 DR Pfam: PF02538; Hydantoinase_B; 1.
 KW Plasmid.
 SQ SEQUENCE 550 AA; 59345 MW; 73E3208B03886CF8 CRC64;

Query Match 70.7%; Score 41; DB 2; Length 550;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSFTDYF 8
 |||||
 Db 231 YSFTDYF 237

RESULT 13

Q96LU7 PRELIMINARY; PRT; 275 AA.
 AC Q96LU7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CDNA FLJ25056 fis, clone CBL04463.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CEREBELLUM;
 RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
 RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
 RA Kawakami B., Nagai K., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK057785; BAB71571.1; -;
 SQ SEQUENCE 275 AA; 31228 MW; 74EF60D529BA27BB CRC64;

Query Match 69.0%; Score 40; DB 4; Length 275;
 Best Local Similarity 70.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYSFTDYFIY 10
 | |||||
 Db 260 GIFFTDYFFY 269

RESULT 14

O63624 PRELIMINARY; PRT; 310 AA.
 AC O63624;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit 1.
 GN NDI.
 OS Dalbulus cimmyti.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Membracoidea; Cicadellidae; Deltocephalinae; Dalbulus.
 OX NCBI_TaxID=74060;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
 RA Nault L.R.;
 RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
 Phylogeny based on Mitochondrial DNA sequences.";
 RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
 CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
 DR EMBL; AF051290; AAC05754.1; -;
 DR InterPro: IPR001694; Resp_NADH_dhl.
 DR Pfam: PF00146; NADHdh; 1.
 DR PROSITE; PS00667; COMPLEX1_NDI_1; 1.
 DR PROSITE; PS00668; COMPLEX1_NDI_2; 1.
 KW Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
 SQ SEQUENCE 310 AA; 36056 MW; FFF22BB436C442F5 CRC64;

Query Match 69.0%; Score 40; DB 8; Length 310;
 Best Local Similarity 77.8%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
 |||||
 Db 160 YSFMDYFSY 168

RESULT 15

O63626 PRELIMINARY; PRT; 310 AA.
 AC O63626;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit 1.
 GN NDI.
 OS Dalbulus elimatus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Membracoidea; Cicadellidae; Deltocephalinae; Dalbulus.
 OX NCBI_TaxID=74070;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
 RA Nault L.R.;
 RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
 Phylogeny based on Mitochondrial DNA sequences.";
 RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
 CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
 DR EMBL; AF051292; AAC05756.1; -;
 DR InterPro: IPR001694; Resp_NADH_dhl.
 DR Pfam: PF00146; NADHdh; 1.
 DR PROSITE; PS00667; COMPLEX1_NDI_1; 1.
 DR PROSITE; PS00668; COMPLEX1_NDI_2; 1.
 KW Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
 SQ SEQUENCE 310 AA; 36327 MW; 4C8E3BDF2C0A38AE CRC64;

Query Match 69.0%; Score 40; DB 8; Length 310;
 Best Local Similarity 77.8%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YSFTDYFIY 10
 |||||
 Db 160 YSFLDYFSY 168

Search completed: March 10, 2003, 17:00:12
 Job time : 24.069 secs

KW Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
SQ SEQUENCE 310 AA; 36155 MW; 14947809CAALB4B1 CRC64;

Query Match 70.7%; Score 41; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YSFDTDFYIY 10
||| ||| I
Db 160 YSFMDYFYIY 168

RESULT 9

ID O63635 PRELIMINARY; PRT; 310 AA.
AC O63635;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
OS Baldulus tripsaci.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracoidea; Cicadellidae; Deltocephalinae; Balduius.
OX NCBI_TaxID=74058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPECIMEN TWO;
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Balbulus leafhopper (Homoptera: Cicadellidae)
Phylogeny based on Mitochondrial DNA sequences.";
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
DR EMBL; AF051301; AAC05765.1; -;
DR InterPro: IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADRDh; 1.
DR PROSITE; PS00668; COMPLEX1_NDL_2; 1.
KW Mitochondrion.
SQ SEQUENCE 310 AA; 36364 MW; C464DF7484DB66E7 CRC64;

Query Match 70.7%; Score 41; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YSFDTDFYIY 10
||| ||| I
Db 160 YSFMDYFYIY 168

RESULT 10

ID O63636 PRELIMINARY; PRT; 310 AA.
AC O63636;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
OS Baldulus tripsaci.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracoidea; Cicadellidae; Deltocephalinae; Balduius.
OX NCBI_TaxID=74058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPECIMEN TWO;
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Balbulus leafhopper (Homoptera: Cicadellidae)
Phylogeny based on Mitochondrial DNA sequences.";
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
DR EMBL; AF051302; AAC05766.1; -;

DR InterPro: IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADRDh; 1.
DR PROSITE; PS00668; COMPLEX1_NDL_2; 1.
KW Mitochondrion.
SQ SEQUENCE 310 AA; 36519 MW; CE7B3A4CA4B5FE70 CRC64;

Query Match 70.7%; Score 41; DB 8; Length 310;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YSFDTDFYIY 10
||| ||| I
Db 160 YSFMDYFYIY 168

RESULT 11

ID Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -;
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 70.7%; Score 41; DB 11; Length 481;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTDYFIY 10
||| ||| I:
Db 45 GYTFTSYVIH 54

RESULT 12

ID O50266 PRELIMINARY; PRT; 550 AA.
AC O50266;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Agag.
GN AGAG.
OS Agrobacterium tumefaciens.
OG Plasmid Ti.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99141607; PubMed=99871134;
RA Lyl S.M., Jafr S., Winans S.C.;
RT "Mannopinic acid and agropinic acid catabolism region of the octopine-
type Ti plasmid pTi15955.";
RL Mol. Microbiol. 31:339-347(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
RA Farrand S.K.;

```

OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225174; CAB65237.1; -
DR HSP: P01810; 2PBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 72.4%; Score 42; DB 11; Length 117;
Best Local Similarity 66.7%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSTFDYFI 9
||:||||:
Db 26 GYTFTDYYM 34

RESULT 6
Q5NT3 PRELIMINARY; PRT; 586 AA.
AC Q5NT3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Similar to Arabidopsis thaliana DNA chromosome 4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0538C01.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP000391; BAAB3364.1; -
DR InterPro: IPR004331; SPX.
DR Pfam: PF03105; SPX; 1.
SQ SEQUENCE 586 AA; 65924 MW; DA2D51DCBFD8C929 CRC64;

Query Match 72.4%; Score 42; DB 10; Length 586;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSTFDYFI 9
||:||||:
Db 136 GYFTDIY 144

RESULT 7
Q8X429 PRELIMINARY; PRT; 253 AA.
AC Q8X429;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ARAC-type regulatory protein.
GN Z2209 OR ECS2104.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.

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OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posafai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL: AE005355; AAG56269.1; -
DR EMBL: AP002557; BAB35527.1; -
DR InterPro: IPR000005; HTHArac.
DR Pfam: PF00165; HTH_Arac; 2.
DR PRINTS: PR00032; HTHARAC.
DR SMART: SM00342; HTH_ARAC; 1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
KW Complete proteome.
SQ SEQUENCE 253 AA; 28885 MW; E77C92CDAC94B9CC CRC64;

Query Match 70.7%; Score 41; Length 253;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYSTFDYFI 10
||:||||
Db 208 GYSTSYFIY 217

RESULT 8
Q63625 PRELIMINARY; PRT; 310 AA.
AC Q63625;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1.
GN NDI.
OS Dalbulus ebberti.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Membracidae; Cicadellidae; Deltocephalinae; Dalbulus.
OX NCBI_TaxID=74061;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich C.H., Fitzgerald S.J., Holmes J.L., Black W.C. IV,
RA Nault L.R.;
RT "Reassessment of Dalbulus leafhopper (Homoptera: Cicadellidae)
Phylogeny based on Mitochondrial DNA sequences.";
RL Ann. Entomol. Soc. Amer. 91:590-597(1998).
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
DR EMBL: AF051291; AAC05755.1; -
DR InterPro: IPR001694; Resp_NADH_dhl.
DR Pfam: PF00146; NADHdh; 1.
DR PROSITE: PS00667; COMPLEX1_NDI_1; 1.
DR PROSITE: PS00668; COMPLEX1_NDI_2; 1.

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